

FIG. 1

PROTEIN ALIGNMENT OF MOUSE, HUMAN AND RAT Nav1.3

mNav1.3 wild-type	(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK
hNav1.3_NM_006922	(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK
hNav1.3_AF225986	(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK
rNav1.3_NM_013119	(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK
mNav1.3 wild-type	(51)	PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF
hNav1.3_NM_006922	(51)	PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF
hNav1.3_AF225986	(51)	PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF
rNav1.3_NM_013119	(51)	PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF
mNav1.3 wild-type	(101)	RFSATSALYILTPINPVRKIAKILVHSLFSLIMCTILTNCVFMTLSP
hNav1.3_NM_006922	(101)	RFSATSALYILTPINPVRKIAKILVHSLFSLIMCTILTNCVFMTLSP
hNav1.3_AF225986	(101)	RFSATSALYILTPINPVRKIAKILVHSLFSLIMCTILTNCVFMTLSP
rNav1.3_NM_013119	(101)	RFSATSALYILTPINPVRKIAKILVHSLFSLIMCTILTNCVFMTLSP
mNav1.3 wild-type	(151)	PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLDPSVIM
hNav1.3_NM_006922	(151)	PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLDPSVIM
hNav1.3_AF225986	(151)	PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLDPSVIM
rNav1.3_NM_013119	(151)	PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLDPSVIM
mNav1.3 wild-type	(201)	AYVTEFVDLGNVSALRTRFVRALKTI SVIPGLKTI VGALIQSVKKLSDV
hNav1.3_NM_006922	(201)	AYVTEFVDLGNVSALRTRFVRALKTI SVIPGLKTI VGALIQSVKKLSDV
hNav1.3_AF225986	(201)	AYVTEFVDLGNVSALRTRFVRALKTI SVIPGLKTI VGALIQSVKKLSDV
rNav1.3_NM_013119	(201)	AYVTEFVDLGNVSALRTRFVRALKTI SVIPGLKTI VGALIQSVKKLSDV
mNav1.3 wild-type	(251)	MILTVFCLSVFALIGLQLFMGNLNRKCLQWPPSDSAFEINTTSYFNGTMD
hNav1.3_NM_006922	(251)	MILTVFCLSVFALIGLQLFMGNLNRKCLQWPPSDSAFEINTTSYFNGTMD
hNav1.3_AF225986	(251)	MILTVFCLSVFALIGLQLFMGNLNRKCLQWPPSDSAFEINTTSYFNGTMD
rNav1.3_NM_013119	(251)	MILTVFCLSVFALIGLQLFMGNLNRKCLQWPPSDSAFEINTTSYFNGTMD

FIG. 1

mNav1.3 wild-type	(301)	SNGTFVNVITMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
hNav1.3_NM_006922	(301)	SNGTFVNVITMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
hNav1.3_AF225986	(301)	SNGTFVNVITMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
rNav1.3_NM_013119	(301)	SNGTFVNVITMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
mNav1.3 wild-type	(351)	ICVKAGRNPNGYTSFDTSWAFSLSLFRLMTQDYWENLYQLTLRAAGKTY
hNav1.3_NM_006922	(351)	ICVKAGRNPNGYTSFDTSWAFSLSLFRLMTQDYWENLYQLTLRAAGKTY
hNav1.3_AF225986	(351)	ICVKAGRNPNGYTSFDTSWAFSLSLFRLMTQDYWENLYQLTLRAAGKTY
rNav1.3_NM_013119	(351)	ICVKAGRNPNGYTSFDTSWAFSLSLFRLMTQDYWENLYQLTLRAAGKTY
mNav1.3 wild-type	(401)	MIFFVLVIFLGSFYLVNLIILAVVAMAYEEQNQATLEEAEOKEAEFQOMLE
hNav1.3_NM_006922	(401)	MIFFVLVIFLGSFYLVNLIILAVVAMAYEEQNQATLEEAEOKEAEFQOMLE
hNav1.3_AF225986	(401)	MIFFVLVIFLGSFYLVNLIILAVVAMAYEEQNQATLEEAEOKEAEFQOMLE
rNav1.3_NM_013119	(401)	MIFFVLVIFLGSFYLVNLIILAVVAMAYEEQNQATLEEAEOKEAEFQOMLE
mNav1.3 wild-type	(451)	QLKKQOEAAQAVAAASASRDFTSCGGELGELLESSSEASKLSSKAKEMR
hNav1.3_NM_006922	(451)	QLKKQOEAAQAVAAASASRDFTSCGGELGELLESSSEASKLSSKAKEMR
hNav1.3_AF225986	(451)	QLKKQOEAAQAVAAASASRDFTSCGGELGELLESSSEASKLSSKAKEMR
rNav1.3_NM_013119	(451)	QLKKQOEAAQAVAAASASRDFTSCGGELGELLESSSEASKLSSKAKEMR
mNav1.3 wild-type	(501)	NRRKKRRQREHLEGNHPEGDRFPKSESEDSVKRRSFLISDGNPLIGDK
hNav1.3_NM_006922	(501)	NRRKKRRQREHLEGNHPEGDRFPKSESEDSVKRRSFLISDGNPLIGDK
hNav1.3_AF225986	(501)	NRRKKRRQREHLEGNHPEGDRFPKSESEDSVKRRSFLISDGNPLIGDK
rNav1.3_NM_013119	(501)	NRRKKRRQREHLEGNHPEGDRFPKSESEDSVKRRSFLISDGNPLIGDK
mNav1.3 wild-type	(551)	KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST
hNav1.3_NM_006922	(551)	KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST
hNav1.3_AF225986	(551)	KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST
rNav1.3_NM_013119	(551)	KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST

FIG. 1

mNav1.3 wild-type	(601)	FEDSESRRDLSLFVPHR	GERRNSVNSQASMSRRMVPGLPANGKMHSTVDC
hNav1.3_NM_006922	(601)	FEDGESRRDLSLFVPHR	HGERRNSVNSQASMSRRMVPGLPANGKMHSTVDC
hNav1.3_AF225986	(601)	FEDSESRRDLSLFVPHR	HGERRNS
rNav1.3_NM_013119	(601)	FEDSESRRDLSLFVPHR	GERRNS
mNav1.3 wild-type	(651)	NGVVSIL	-----GTTTETEVKRRLLSSYOISMEMLEDSS
hNav1.3_NM_006922	(651)	NGVVSILVGGPSALTSPTGQLP	EGTTTETEVKRRLLSSYOISMEMLEDSS
hNav1.3_AF225986	(625)	-----	-----GTTTETEVKRRLLSSYOISMEMLEDSS
rNav1.3_NM_013119	(625)	-----	-----GTTTETEVKRRLLSSYOISMEMLEDSS
mNav1.3 wild-type	(684)	GRQRANSIASILNTNMEEL	ESRQKCPPCWYRFANVFLIWDCCD
hNav1.3_NM_006922	(701)	GRQRANSIASILNTNMEEL	ESRQKCPPCWYRFANVFLIWDCCD
hNav1.3_AF225986	(652)	GRQRANSIASILNTNMEEL	ESRQKCPPCWYRFANVFLIWDCCD
rNav1.3_NM_013119	(652)	GRQRANSIASILNTNMEEL	ESRQKCPPCWYRFANVFLIWDCCD
mNav1.3 wild-type	(734)	HLVNLIVMDPFVDL	LAITICIVLNTLFWAMEHYPMTEQFSSVLT
hNav1.3_NM_006922	(751)	HLVNLIVMDPFVDL	LAITICIVLNTLFWAMEHYPMTEQFSSVLT
hNav1.3_AF225986	(702)	HLVNLIVMDPFVDL	LAITICIVLNTLFWAMEHYPMTEQFSSVLT
rNav1.3_NM_013119	(702)	HLVNLIVMDPFVDL	LAITICIVLNTLFWAMEHYPMTEQFSSVLT
mNav1.3 wild-type	(784)	GIFTAEMVLKIIANDP	PYYFQEGWNIFDGIIVSLSLMELGLINVEGLSVL
hNav1.3_NM_006922	(801)	GIFTAEMVLKIIANDP	PYYFQEGWNIFDGIIVSLSLMELGLINVEGLSVL
hNav1.3_AF225986	(752)	GIFTAEMVLKIIANDP	PYYFQEGWNIFDGIIVSLSLMELGLINVEGLSVL
rNav1.3_NM_013119	(752)	GIFTAEMVLKIIANDP	PYYFQEGWNIFDGIIVSLSLMELGLINVEGLSVL
mNav1.3 wild-type	(834)	RSFRLIRVFKLAKSW	PTLNMLIKIIGNSVGALGNLTIVLALIVFIFAVVG
hNav1.3_NM_006922	(851)	RSFRLIRVFKLAKSW	PTLNMLIKIIGNSVGALGNLTIVLALIVFIFAVVG
hNav1.3_AF225986	(802)	RSFRLIRVFKLAKSW	PTLNMLIKIIGNSVGALGNLTIVLALIVFIFAVVG
rNav1.3_NM_013119	(802)	RSFRLIRVFKLAKSW	PTLNMLIKIIGNSVGALGNLTIVLALIVFIFAVVG
mNav1.3 wild-type	(884)	MQLFGKSYKEVCVKIN	DCKLPRWHMNDFFHSFLIVRVLGGEWETMWD

FIG. 1

hNav1.3_NM_006922	(901)	MQLFGKSYKECVCKINDDCQLPRWHMNDFFHSFLIVFRVLGGEWIEIETMWD
hNav1.3_AF225986	(852)	MQLFGKSYKECVCKINDDCQLPRWHMNDFFHSFLIVFRVLGGEWIEIETMWD
rNav1.3_NM_013119	(852)	MQLFGKSYKECVCKINDVDCGLPRWHMNDFFHSFLIVFRVLGGEWIEIETMWD
mNav1.3 wild-type	(934)	CMEVAGQTMCLIVFVLMVMVIGNLVVLNLFALLLSFSFSDNLAATDDNE
hNav1.3_NM_006922	(951)	CMEVAGQTMCLIVFVLMVMVIGNLVVLNLFALLLSFSFSDNLAATDDNE
hNav1.3_AF225986	(902)	CMEVAGQTMCLIVFVLMVMVIGNLVVLNLFALLLSFSFSDNLAATDDNE
rNav1.3_NM_013119	(902)	CMEVAGQTMCLIVFVLMVMVIGNLVVLNLFALLLSFSFSDNLAATDDNE
mNav1.3 wild-type	(984)	MNNLQIAVGRMOKGIDVKNKRECFKAFRKPVKVIEIEGKNKIDSCMS
hNav1.3_NM_006922	(1001)	MNNLQIAVGRMOKGIDVKNKRECFKAFRKPVKVIEIEGKNKIDSCMS
hNav1.3_AF225986	(952)	MNNLQIAVGRMOKGIDVKNKRECFKAFRKPVKVIEIEGKNKIDSCMS
rNav1.3_NM_013119	(952)	MNNLQIAVGRMOKGIDVKNKRECFKAFRKPVKVIEIEGKNKIDSCMS
mNav1.3 wild-type	(1034)	NNTC-EISKELNVLGDNGTTSVGTGSSVEKVIIDENDYMSFINNPSL
hNav1.3_NM_006922	(1051)	NNTC-EISKELNVLGDNGTTSVGTGSSVEKVIIDENDYMSFINNPSL
hNav1.3_AF225986	(1002)	NNTGT-EISKELNVLGDNGTTSVGTGSSVEKVIIDENDYMSFINNPSL
rNav1.3_NM_013119	(1002)	NNTGT-EISKELNVLGDNGTTSVGTGSSVEKVIIDENDYMSFINNPSL
mNav1.3 wild-type	(1084)	TVTVP IAVGESDFENLNTFEFSSELEESKEKINATSSSEGSTVDVLP
hNav1.3_NM_006922	(1100)	TVTVP IAVGESDFENLNTFEFSSELEESKEKINATSSSEGSTVDVLP
hNav1.3_AF225986	(1051)	TVTVP IAVGESDFENLNTFEFSSELEESKEKINATSSSEGSTVDVLP
rNav1.3_NM_013119	(1051)	TVTVP IAVGESDFENLNTFEFSSELEESKEKINATSSSEGSTVDVLP
mNav1.3 wild-type	(1134)	REGQAEIPEEDFKPEACFTGECIKKFPFCQVSTEEGKGKIWNLRKTC
hNav1.3_NM_006922	(1150)	REGQAEIPEEDFKPEACFTGECIKKFPFCQVSTEEGKGKIWNLRKTC
hNav1.3_AF225986	(1101)	REGQAEIPEEDFKPEACFTGECIKKFPFCQVSTEEGKGKIWNLRKTC
rNav1.3_NM_013119	(1101)	REGQAEIPEEDFKPEACFTGECIKKFPFCQVSTEEGKGKIWNLRKTC
mNav1.3 wild-type	(1184)	YSIVEHNWFETPLVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY
hNav1.3_NM_006922	(1200)	YSIVEHNWFETPLVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY

FIG. 1

hNav1.3_AF225986	(1151)	YSIVEHNNFFETFIIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFY
rNav1.3_NM_013119	(1151)	YSIVEHNNFFETFIIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFY
mNav1.3 wild-type	(1234)	IFILEMILLKWAYGFGQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA
hNav1.3_NM_006922	(1250)	IFILEMILLKWAYGFGQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA
hNav1.3_AF225986	(1201)	IFILEMILLKWAYGFGQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA
rNav1.3_NM_013119	(1201)	IFILEMILLKWAYGFGQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA
mNav1.3 wild-type	(1284)	IKSLRTLRALRPLRALSRFEGMRVNVNALVGAIPIIMNVLLVCLIFWLIF
hNav1.3_NM_006922	(1300)	IKSLRTLRALRPLRALSRFEGMRVNVNALVGAIPIIMNVLLVCLIFWLIF
hNav1.3_AF225986	(1251)	IKSLRTLRALRPLRALSRFEGMRVNVNALVGAIPIIMNVLLVCLIFWLIF
rNav1.3_NM_013119	(1251)	IKSLRTLRALRPLRALSRFEGMRVNVNALVGAIPIIMNVLLVCLIFWLIF
mNav1.3 wild-type	(1334)	SIMGVNLFAGKFYHCVNMTTGNMFDISKVNNFSDCOALGKQARWKNVKVN
hNav1.3_NM_006922	(1350)	SIMGVNLFAGKFYHCVNMTTGNMFDISKVNNFSDCOALGKQARWKNVKVN
hNav1.3_AF225986	(1301)	SIMGVNLFAGKFYHCVNMTTGNMFDISKVNNFSDCOALGKQARWKNVKVN
rNav1.3_NM_013119	(1301)	SIMGVNLFAGKFYHCVNMTTGNMFDISKVNNFSDCOALGKQARWKNVKVN
mNav1.3 wild-type	(1384)	FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV
hNav1.3_NM_006922	(1400)	FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV
hNav1.3_AF225986	(1351)	FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV
rNav1.3_NM_013119	(1351)	FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV
mNav1.3 wild-type	(1434)	IFILFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYINAMKKL
hNav1.3_NM_006922	(1450)	IFILFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYINAMKKL
hNav1.3_AF225986	(1401)	IFILFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYINAMKKL
rNav1.3_NM_013119	(1401)	IFILFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYINAMKKL
mNav1.3 wild-type	(1484)	GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD
hNav1.3_NM_006922	(1500)	GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD
hNav1.3_AF225986	(1451)	GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD

FIG. 1

rNav1.3_NM_013119	(1451)	GSKPKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVMMVETDD
mNav1.3 wild-type	(1534)	QKYM TL VL SR INL VF IVLFTGEF IL KL SLR YYFTTIGNIFDFV V IL
hNav1.3_NM_006922	(1550)	Q Q KYMTLVLSRINL VF IVLFTGEF IL KL SLR YYFTTIGNIFDFV V IL
hNav1.3_AF225986	(1501)	Q Q KYMTLVLSRINL VF IVLFTGEF IL KL SLR YYFTTIGNIFDFV V IL
rNav1.3_NM_013119	(1501)	Q Q KYMTLVLSRINL VF IVLFTGEF IL KL SLR YYFTTIGNIFDFV V IL
mNav1.3 wild-type	(1584)	SIVGMFLA E IEKYFVSPTLFRVIRLARI GR ILRLIKGAKGIRTL L FALM
hNav1.3_NM_006922	(1600)	SIVGMFLA E IEKYFVSPTLFRVIRLARI GR ILRLIKGAKGIRTL L FALM
hNav1.3_AF225986	(1551)	SIVGMFLA E IEKYFVSPTLFRVIRLARI GR ILRLIKGAKGIRTL L FALM
rNav1.3_NM_013119	(1551)	SIVGMFLA E IEKYFVSPTLFRVIRLARI GR ILRLIKGAKGIRTL L FALM
mNav1.3 wild-type	(1634)	MSLPALFNIGLILLFLVMFIYALFGMSNFAYV Y KEAGIDDMFN F ETFGNSM
hNav1.3_NM_006922	(1650)	MSLPALFNIGLILLFLVMFIYALFGMSNFAYV Y KEAGIDDMFN F ETFGNSM
hNav1.3_AF225986	(1601)	MSLPALFNIGLILLFLVMFIYALFGMSNFAYV Y KEAGIDDMFN F ETFGNSM
rNav1.3_NM_013119	(1601)	MSLPALFNIGLILLFLVMFIYALFGMSNFAYV Y KEAGIDDMFN F ETFGNSM
mNav1.3 wild-type	(1684)	ICLFQITTSAGWDGHLAPILNSAP PD CDPDAIHPGSSVKGDCG PS VGIF
hNav1.3_NM_006922	(1700)	ICLFQITTSAGWDGHLAPILNSAP PD CDPDAIHPGSSVKGDCG PS VGIF
hNav1.3_AF225986	(1651)	ICLFQITTSAGWDGHLAPILNSAP PD CDPDAIHPGSSVKGDCG PS VGIF
rNav1.3_NM_013119	(1651)	ICLFQITTSAGWDGHLAPILNSAP PD CDPDAIHPGSSVKGDCG PS VGIF
mNav1.3 wild-type	(1734)	FFVS Y IIISFLV V VMNYIAVILENFSVATER SA EPLSEDDFEMFYEV W EK
hNav1.3_NM_006922	(1750)	FFVS Y IIISFLV V VMNYIAVILENFSVATER SA EPLSEDDFEMFYEV W EK
hNav1.3_AF225986	(1701)	FFVS Y IIISFLV V VMNYIAVILENFSVATER SA EPLSEDDFEMFYEV W EK
rNav1.3_NM_013119	(1701)	FFVS Y IIISFLV V VMNYIAVILENFSVATER SA EPLSEDDFEMFYEV W EK
mNav1.3 wild-type	(1784)	FDPDATQFIEFC KL SDFAAALDP PLL IAKPNKVQLIAMDLPMVSGDR I HC
hNav1.3_NM_006922	(1800)	FDPDATQFIEFC KL SDFAAALDP PLL IAKPNKVQLIAMDLPMVSGDR I HC
hNav1.3_AF225986	(1751)	FDPDATQFIEFC KL SDFAAALDP PLL IAKPNKVQLIAMDLPMVSGDR I HC
rNav1.3_NM_013119	(1751)	FDPDATQFIEFC KL SDFAAALDP PLL IAKPNKVQLIAMDLPMVSGDR I HC

FIG. 1

mNav1.3 wild-type	(1834)	LDILFAFTKRVLCESGEMDALRIQMEDRFMASNP	SKVSYEPITTTTLKRQ
hNav1.3_NM_006922	(1850)	LDILFAFTKRVLCESGEMDALRIQMEDRFMASNP	SKVSYEPITTTTLKRQ
hNav1.3_AF225986	(1801)	LDILFAFTKRVLCESGEMDALRIQMEDRFMASNP	SKVSYEPITTTTLKRQ
rNav1.3_NM_013119	(1801)	LDILFAFTKRVLCESGEMDALRIQMEDRFMASNP	SKVSYEPITTTTLKRQ
mNav1.3 wild-type	(1884)	EEVSAAIQRNRCVLLKQRLKNISNTYDKH	IKGRIVLPKGDMAIDKL
hNav1.3_NM_006922	(1900)	EEVSAAIQRNRCVLLKQRLKNISNTYDKH	IKGRIVLPKGDMAIDKL
hNav1.3_AF225986	(1851)	EEVSAAIQRNRCVLLKQRLKNISNTYDKH	IKGRIVLPKGDMAIDKL
rNav1.3_NM_013119	(1851)	EEVSAAIQRNRCVLLKQRLKNISNTYDKH	IKGRIVLPKGDMAIDKL
mNav1.3 wild-type	(1934)	NGNSTPEKTDGSSSTTTPPSYDSVT	KPDKEKFEKDKPEKSKGKEV----
hNav1.3_NM_006922	(1950)	NGNSTPEKTDGSSSTTTPPSYDSVT	KPDKEKFEKDKPEKSKGKEVRENQ
hNav1.3_AF225986	(1901)	NGNSTPEKTDGSSSTTTPPSYDSVT	KPDKEKFEKDKPEKSKGKEVRENQ
rNav1.3_NM_013119	(1901)	NGNSTPEKTDGSSSTTTPPSYDSVT	KPDKEKFEKDKPEKSKGKEVRENQ
mNav1.3 wild-type	(1980)	--	
hNav1.3_NM_006922	(2000)	K-	
hNav1.3_AF225986	(1951)	K-	
rNav1.3_NM_013119	(1951)	K-	

FIG. 2

ALIGNMENT OF FULL-LENGTH AND PARTIAL MOUSE Nav1.3 PROTEIN

mNav1.3 wild-type	(1)	MAQALLVPPGPSPSFRLLFTRESLAAIEKRAAEKAKKPKKE
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(41)	QDIDENKPKNSDLEAGKNLPFIYGDIPPEMVSEPLEDL
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(81)	DPYVSKKTFVVLNKGKAIFFRSATSALYILTPLNPVKKI
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(121)	AIKILVHSLFSLIMCTILTNCVFMTLSPDPDWTKNVEYT
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(161)	FTGIYTFESLIKILARGFCLEDFTELRDPWNWLDFSVIVM
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(201)	AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIIVGAL
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(241)	IQSVKKLSDVMLITVFCLSVFALIGLQLFMGNI RNKCLOW
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(281)	PPSDSAFEINTSYFNGMTDSNGTFFVNVMTSTFNWKDYIA
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(321)	DDSHFYVLDGQKDPILLCGNGSDAGQCPEGYICVKAGRPN
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(361)	YGYSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
mNav1.3 NM_018732		-----

FIG. 2

mNav1.3 wild-type mNav1.3 NM_018732	(401) MIEFFLVIFLGSFYLVNLLILAVVAMAYEEQNQATLEEAEQ -----
mNav1.3 wild-type mNav1.3 NM_018732	(441) KEAEFQQMLEQLKKQEEAQAVAAASAASRDFSGIGGLGE -----
mNav1.3 wild-type mNav1.3 NM_018732	(481) LLESSEASKLSSKSAKEWNRKRKRRQREHLEGNHRPEG -----
mNav1.3 wild-type mNav1.3 NM_018732	(521) DRFPKSESEDSVKRRSFLFSLDGNPLSGDKKLCSPHQSIIL -----
mNav1.3 wild-type mNav1.3 NM_018732	(561) SIRGSLFSPRNSKTSIFSFRGRAKDVGSENFADDEHST -----
mNav1.3 wild-type mNav1.3 NM_018732	(601) FEDSESRDLSLFVPHRPGERRNSNVSQASMSRMPGLPA -----
mNav1.3 wild-type mNav1.3 NM_018732	(641) NGKMHSTVDCNGVVSIGTTTETEVKRRRLSSYQISMEMLE -----
mNav1.3 wild-type mNav1.3 NM_018732	(681) DSSGRQAMSTASILTNTMEELEESRQKCPPCWYRFANVF -----
mNav1.3 wild-type mNav1.3 NM_018732	(721) LIWDCCDSWLKVKHLVNLIVMDPFVDLAIICIVLNTLFM -----
mNav1.3 wild-type mNav1.3 NM_018732	(761) AMEHYPMTEQFSVLTVGNLVFTGIFTAEWVLKIIAMDPY -----
mNav1.3 wild-type mNav1.3 NM_018732	(801) YYFQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLIR -----

FIG. 2

mNav1.3 wild-type	(841)	VFKIAKSWPTLNMLIKIGNSVGALGNLTILVLAIIIVFIFA
mNav1.3 NM_018732	(1)	-----MLIKIGNSVGALGNLTILVLAIIIVFIFA
mNav1.3 wild-type	(881)	VVGQQLFGKSYKEVCCKINEDCKLPRWHMNDFFHSFLIVF
mNav1.3 NM_018732	(29)	VVGQQLFGKSYKEVCCKINEDCKLPRWHMNDFFHSFLIVF
mNav1.3 wild-type	(921)	RVLCGEWIEIWMDCMEVAGQTMCLIVFVLMVMVIGNLVILN
mNav1.3 NM_018732	(69)	RVLCGEWIEIWMDCMEVAGQTMCLIVFVLMVMVIGNLVILN
mNav1.3 wild-type	(961)	LFLALLSSFSDDNLAATDDDNEMNNLQIAVGRMOKGIDY
mNav1.3 NM_018732	(109)	LFLALLSSFSDDNLAATDDDNEMNNLQIAVGRMOKGIDY
mNav1.3 wild-type	(1001)	VKNKIRECFRKAFRRKPKVIEIHGKNKIDSCMSNNTGVVE
mNav1.3 NM_018732	(149)	VKNKIRECFRKAFRRKPKVIEIHGKNKIDSCMSNNTGVVE
mNav1.3 wild-type	(1041)	ISKELNYLKDNGTTSVGVTGSSVEKVIIDENDYMSFINN
mNav1.3 NM_018732	(189)	ISKELNYLKDNGTTSVGVTGSSVEKVIIDENDYMSFINN
mNav1.3 wild-type	(1081)	PSLTIVTVPIAVGESDFENLNTTEFFSSESELESKEKLNAT
mNav1.3 NM_018732	(229)	PSLTIVTVPIAVGESDFENLNTTEFFSSESELESKEVSALF
mNav1.3 wild-type	(1121)	SSSEGSTVDVAPPREGEQAEPEEDLKPEACFTEGCIKK
mNav1.3 NM_018732	(269)	SSGHHFCAIYTVWLLCIVFC-----
mNav1.3 wild-type	(1161)	FPFCQVSTEEGKGKIWNLRKTCYSIVEHNNWFETFIIVFMI
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1201)	ILSSGALAFEDIYIEHQRTIKTMLEYADKVFTYIFILEML
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1241)	LKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSE
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1281)	LGAIKSLRTILRALRPLRALSRFEGMRVVVNALVGAIPSIM

FIG. 2

mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1321)	NVLLVCLIFWLIFSIMGVNLFAGKFYHCVMNMTTGSMTDMS
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1361)	EVNNSDCQALGKQARWKNVKNFDNVGAGYLALLQVATF
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1401)	KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGS
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1441)	FFTILNFIGVIIDNFNQKKKGGQDIFMTEEQKKYYNAM
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1481)	KKLGSKKPQKPIPRPANKFOGMVDFVTRQVFDISIMILI
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1521)	CLNMVTMMVETDDQSKYMTLVLSRINLVFIVLFTGEFLIK
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1561)	LISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1601)	PTLFRVIRLARIGRILRLIKGAKGIRTLILFALMMSLPALF
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1641)	NIGLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFTFG
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1681)	NSMICLFQITTSAGWDGILLAPILNSAPPDPCDPAIHPCSS
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1721)	VKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSV
mNav1.3 NM_018732		-----

FIG. 2

mNav1.3 wild-type	(1761)	ATERSAEPLSEDDFEMFYEVWEKFDPDATQFIEFCKLSDF
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1801)	AAALDPPLLIAPKNKVQLIAMDLPMVSGDRIHCLDILFAF
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1841)	TKRVLGESGEMDALRIQMEDREFMASNPISKVSEPIITTLK
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1881)	RKQEEVSAAIIQRNYRCYLLKQRLKNISNTYDKETIKGRI
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1921)	VLPIKGDWVIDKLNNGNSTPEKTDGSSSTTSPPSYDSVTKP
mNav1.3 NM_018732		-----
mNav1.3 wild-type	(1961)	DKEKFEKDKPEKESKGKEV
mNav1.3 NM_018732		-----

FIG. 3

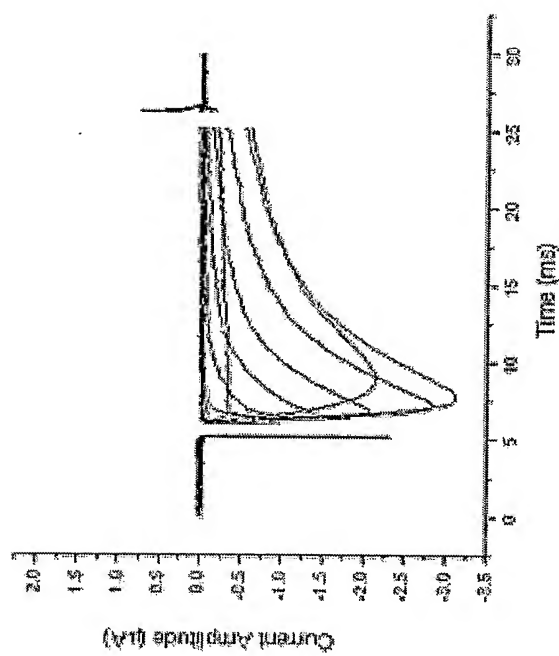


FIG. 4

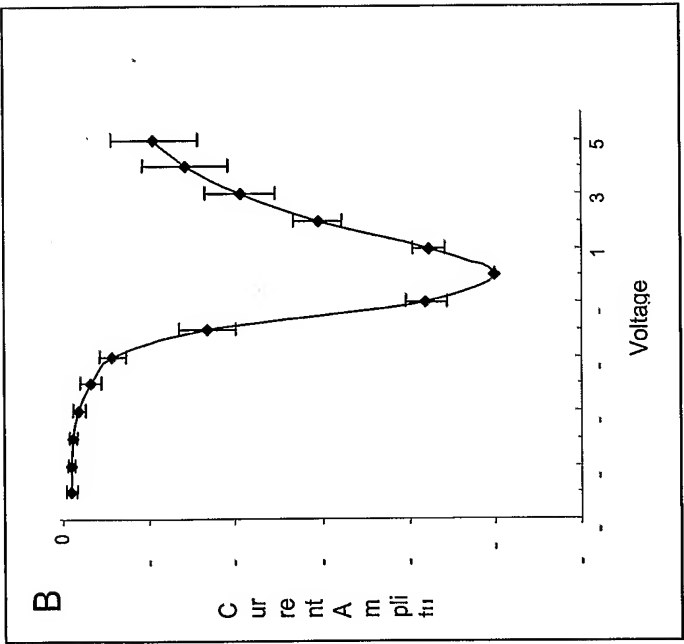


FIG. 5

SEQ ID NO:1

ATGGCCAGGCACTGCTGGTACCCCGGGACCTGAGAGCTTCC
GCCTTTTCACTCGAGAACTCTTGTGCTGCTATCGAAAAAGCGTGTCTGCAGAA
GAGAAAGCCAAAGAAACCCAAAGAAAGAACAGACATTGACGATGAGAACAA
GCCAAAGCCAAACAGTGACTTGGAGCTGGAGAACCTTCCATTATCT
ATGGAGACATTCCTCCAGAGATGGTCTCGAGCCCTCTGGAGGACCTGGAC
CCCTACTACGTCAGTAAGAAAACCTTTGTAGTGTGAATAAAGGGAGGC
AATTTTCGATTCAGTGCACCTCCGCTGTGTATATTTAACTCCACTAA
ACCCCGTTAGGAAAATTGCTATTAAAGATTTGGTACACTCTTTATTTCAGC
ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACATTGAG
CAATCCTCCTGACTGGACGAAGAAATGTAGAGTACACATTCACTGGGATCT
ATACCTTTGAGTCACCTTAFAAAGATCTTGGCCAGAGGATTCGTTAGAA
GATTTCACTTCTTCTGTGACCCATGGAACTGGCTGGATTTCAAGTGTCA
CTGATGGCATATGTGACAGAGTTTGTGACCTGGGCAATGTCTCAGCGC
TGAGAAAGTTTCAGAGTTCTCGAGCATTGAAAAACAATACTAGTCAATCCA
GGTTTAAAGACCATCGTGGGGCCCTGATCCAGTCGGTGAAGAAGCTGTC
TGACGTCAATGATACTCACTGTGTCTGTCTGAGCGTCTTTGCTCTCATCG
GGCTGCAGCTCTTCATGGCAACCTGAGGAATAAATGCTTGCAGTGGCT
CCAAGCGATTCGCTTTTGAGATCAACACTACTTCTACTTCAATGGCAC
AATGGAATCAAAATGGGACATTTGTGTAATGTAACAATGAGCACATTCAACT
GGAAGGACTATATCGCAGATGACAGCCACTTTTATGTTTGGATGGACAA
AAAGATCCTTTACTTTGTGAAAATGGGTCCGATGCAGACAAATGTCCAGA
AGGGTACATCTGTGTGAAGCTGGACGAACCCCACTACGGTTACAGA
GCTTTGACACATTTAGCTGGGCCCTTCTTATCGCTGTTTCGACTCATGACT
CAAGACTACTGGGAGAACCTTTACCAGTTGACATTAACGTGACGTGGGAA
AAGCTACATGATCTTTTCTGTCCTGGTAAATTTTCTTGGGCTCATTTTATT
TGGTGAACTTGTATCTTGGCTGTGGTGGCCATGGCCATGAGGAAACAAAT
CAGGCCACATCGGAGGAGGTGAGCAGAAAGAGGCGGATTTTCAGCAGAT
GTTGGAGCAGTTGAAAGAGCAGAAAGAGGAGGCTCAGGCGGTGGCAGCTG
CCTCAGCAGCGCTCCAGAGACTTCAGTGGGATAGGAGGTTAGGAGAACTT
CTGGAGAGTTCTTCAGAAAGCTTCCAAGTTGAGTCCAAAGAGTGCCAAAGGA
GTGGAGGAATCGGAGGAAGAAAGAGGAGACAGAGGGGACCTTGGAGGGAA

FIG. 5

ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAAATCAGAAAGACAGC
GTCAAGCGAAGGAGTTTCTGTGTTCTCCCTGGATGGGAACCCGCTGAGCGG
CGACAAGAAGCTGTGCTCTCCCATCAGTCTCTCTTGAGTATCCGTGGCT
CCTGTTTCCCAAGACCAATAGCAAAACGAGCATTTTCAGCTTCAGA
GGTCGGCGGAAGGACGTGGGTCTGAGATGACTTTGCGGATGATGAACA
CAGCACCTTTGAAGATAGCAGAGACGAGAGAGACTCACTGTTTGTGCGGC
ACAGACCTGGAGAGCGACGCAACAGTAACGTTAGTCAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCAAATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGTTTCTTGGGTACCAACCACTGAAACAGAAATCA
GGAAGAGAAGGCTAAGTTCTTACCAGATCTCGATGGAAATGCTGGAGGAT
TCCTCTGGGAGACAAAGACCATGAGCATAGCCAGTATCCTGACCAACAC
GATGGAGGAACCTTGAAGATCTAGACAGAAGTGTCCACCATGCTGGTATA
GATTTGCCAATGTGTTTGTGATCTGGGACTGTTGTGATTCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATTTGTGATGGATCCATTTGTTGACCTGGC
CATCACCATCTGTCATCGTGTAAACACACTGTTTCATGGCCATGGAGCACT
ACCCGATAGCGGAGCAGTTTCAGCAGTGTGCTGACGGTGGGAAACCTGGTC
TTCAACGGGATCTTCAAGCCGAGATGGTCTGTGAAATCATCGCAATGGA
TCCCTATTACTATTTCGAAGAGGCTGGAATATCTTTGATGGAAATATTG
TTAGCCTGAGTTTAATGGAGCTTGGCCCTGGCAACCGTGGAGGGGCTGTCC
GTGCTTCGGTCTTTCAGACTGCTCGAGTCTTCAAGTTGGCAAAATCCTG
GCCCACACTGAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCAC
TGGGCAACCTGACCCCTGGTCTGGCCATCATCGTCTTCATTTTGGCGTG
GTCGGCATGAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTGCAAGAT
CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
CCTTCCGTAGTGTTCGCGTGTGTGGGCGCAGACCATGTGCTTATTGTGTTAT
TGGGACTGCATGGAGTCCGGGCGCAGACCATGTGCTTATTGTGTTAT
GTGTGTCATGGTGATTGGAAACCTTGTGTTCTGAACTCTTCTGGCCT
TATTGTTGAGTCTTTAGTTTCAACAACCTTGTGCTACGGACGATGAT
AACGAAATGAAACAACCTCCAGATCGCGTGGGAGGATGCAAAAGGGGAT
TGATTATGTGAAAATAAGATACGGGAGTGTTCGGAAGAGCTTTTAA
GAAAGCCGAAAGTATAGAAATCCACGAAGGGAACAAAATAGACAGCTGC
ATGTCCAATAACACGGGCGTAGTTGAAATAAGCAAGAGCTTAACCTACCT
TAAAGACGGTAACGGAACCAACCACTGGCGTGGGTACTGGAAGCAGTGTGG

FIG. 5

AGAAATACGTAATTGATGAAAAATGACTACATGTTCATTTCATCAACAACCCC
 AGCTCACCGTGACGGTGCCTAATGCGTGGGAGAGTCTGACTTTTGA AAA
 TTTTAAACA CGGAAGAGTTTAGCAGTGAGTCAGAACTGGAAAGAAAGCAAGG
 AGAAATTAAATGCAACCAAGCTCTTTCTGAAGGAAGCACAGTTGACGTTGGCT
 CCGCCCCGAGAGGTGAACAAGCTGAAATGAAACCTGAGGAGGACCTTAA
 GCCAGAAGCTTGTCTTACTGAAGGATGCATTAAAAATTTCCCTTCTGCC
 AAGTAAGTACGGAAGAAGTAAAGGAAAAATCTGGTGAATCTTAGGAAG
 ACCTGCTATAGCATGTGGAACACAACCTGGTTTGAGACCTTCATTGTGTT
 CATGATTCTCCTCAGTAGTGGTGCTTTGGCTTTGAAGATATATACATTG
 AGCAACGGAAGACCATCAAAACCATGTGGAGTATGCTGACAAAAGCTTTC
 ACTTACATCTTTCATCCTGGAAATGCTCCTCAAAATGGGTGGCCTATGGATT
 TCAAAACCTATTTCA CCAATGCCCTGGTCTGGTTGGA CTTCCTTGATTGTTG
 ATGTTCTTTTGGTTAGCTTGGTGGCCACGCTCTTTGGCTATTCAGAACTT
 GGTGCCATCAATCCCTACGACCCCTGAGAGCTCTGAGCGCTCCGAGC
 CTTATCCCGCTTTGAAGGCATGAGGGTGGTTGTGAACGCTCTTGTGGTG
 CAATCCCCTCCATCATGAATGTGCTA CTGGTGTGCCCTCATCTTCTGGTTA
 ATCTTTAGTATCATGGGTGTAATCTGTTTGTCTGGAAGTTCTATCACTG
 TGTAAACATGACAACGGGCAGCATGTTCCACATGAGTGAAGTCAACAATT
 TCAGCGACTGTCAGGCTCTTGGCAAGCAAGCCCGATGGAAGAATGTGAAA
 GTCAACTTTTGACAAATGTTGGGGCTGGCTACCTGGCATTTGCTCAAGTGGC
 CACATTCAAAGGCTGGATGGATATTATGTATGCAGCTGTGGATTCAO GGG
 ACGTCAAACCTGCAGCCTGTATATGAAGAAAATCTGTA CATGTATCTGTAC
 TTTGTTCATCTTTCATCATCTTTGGGTGCTTCTTCACTCTAAATCTATTCA
 CGCGGTCACTATAGACAACCTTCAACCCAGCAGAGAAGAAAGTTTGGAGGTC
 AAGACATCTTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAG
 AAACCTGGCTCCAAAAAACCTCAGAAAGCCATCCCTCGACCTGCAACAA
 ATTTCAAGGAATGGTCTTTGACTTTTGAACCTTGTAAACAGACAAGTGTGACATCA
 GCATCATGATCTCATCTGCCCTCAACATGGTGACCATGATGGTGGAAACG
 GACGACGAGCAAAATACATGACCCCTGGTTTTGTCCCGAATCAACCTGGT
 ATTCATCGTCTCTTCACTGGGGAGTTTCTGCTGAAGTCACTCTCTCA
 GATACTACTACTTCA CGATTTGGCTGGAAACATCTTTGACTTTGTGGTGGTG
 ATTCCTCAATGTAGGAATGTTCCCTGCTGAGCTGATAGAGAAGTATTT
 TGTGTCTCCCTACCTGTTCCGAGTCAATCCGCTTGGCCAGGATTTGGACGAA
 TCCTACGCTGATCAAGGGGCCAAGGGGATCCGCA CGCTGCTCTTTGCT

FIG. 5

CTGATGATGTCCCTTCTCGCTGTTCACACATCGGCCCTCCTGCTTTTCCTT
CGTCATGTTTCATCGCCATCTTGGGATGTCCAACTTTGCCTATGTTA
AAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAAC
AGCATGATCTGCTGTTCCTAAATCACCACCTCTCGGGCTGGGATGGACT
GTTGGCCCCATCCTCAACAGTGCACCTCCTGACTGTGACCCCTGATGCAA
TTCACCCCTGGAAGCTCAGTGAAGGAGACTGTGGGAACCCATCTGTGGGG
ATTTTCTTTTGTGTCAGCTACATCATATATCTTCTCTGTTGTGTGAA
CATGTACATTGCTGTCTCCTGGAGAACTTCAGCGTTGCCACAGAGAAA
GTGCAGAGCCCTGAGTGAGGACGACTTTGAGATGTTTACGAGGTCTGG
GAGAAAGTTCGACCCCTGACGCCACCCAGTTTCATAGAGTTCTGCAAGCTCTC
TGACTTTGCAGCTGCCCTGGATCCTCCCTCCTCATCGCAAGCCAAACA
AAGTCCAGCTCATTTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATC
CACTGCCCTGGACATCTTATTTGCTTTTACAAAGCGGTCCTGGGTGAGAG
TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGGTTTCATGGCTT
CCATCCCTCCAGGTCTCTTATGAGCCCATTACCACCACTCTGAAGGCG
AAACAAGAGGAGGTGTCTGCTGCTATCATTCAGCGTAAATTAAGATGTTA
TCTTTTAAAGCAAGGTTAAAAACATATCAAAATACGTATGACAAAGAGA
CAATCAAGGGGAGGATTTGCTTGCCTATAAAGGAGATATGGTTATTGAC
AAATTAATGGGAATTCACCCAGAAAAGACAGATGGGAGTTCTCTTAC
CACTCCCTCCTTCTATGACAGTGTACAAAACCCAGATAAGGAAAAAGT
TTGAGAAAGACAAAACAGAAAAAGCAAGGAAAGAGGTTCTGA

FIG. 5

SEQ ID NO:2

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKPKKEQDIDDENKPK
 PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYVSKKTFVVLNKGKAIF
 RFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILTNCVFMTLSNP
 PDWTKNVEYTFGTGIYTFESLIKILARGFCLDFTFRLRDPMNWLDVSVIVM
 AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTI VGALIQSVKKLSDV
 MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD
 SNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
 ICVKAGRNPNGYTSFDTFSWAFLSLFRMLMTQDYWENLYQLTLRAAGKTY
 MIFFVLVIFLGSFYLVNLI LAVVAMAYEEQNQATLEEAQKEAEFQQMLE
 QLKQEQEEAQAVAAAASRD FSGIGGIGELLESSEASKLSKSAKEWR
 NRRKKRQREHLEGNHRPEGRFPKSESDSVKRRSFLFSLDGNPLSGDK
 KLCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
 FEDSESRDLSLFVPHRPGERRNSVQASMSRMVPGLPANGKMHSTVDC
 NGVVSIGTTTETETEVRKRRLSSYQISMEMLEDSSGRQRAMSIASILTNTME
 ELEESRQKCPPCWYRFANVFLIWDCCDSWLKVKHIVNLI VMDPFVDLAI T
 ICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGTGIFTAEMVLKIIAMD PY
 YYFQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPT
 LNMLIKIIIGNSVGALNLTIVLAIIVFIFAVVGMQLFGKSYKECVCKINE
 DCKLPRWHMNDFFHSFLIVFRVLCGEWETMWDCEVAGQTMCLIVFMLV
 MVI GNLVVLNLF LALLSSFS SDNLAAATDDDNEMNNLQIAVGRMQKGIDY
 VKNKIRECFRKAFFRKPVIIEHGNKIDSCMSNNTGVVEISKELNYLKD
 GNGTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVP IAVGESDFENLN
 TEEFSSESELEESKEKLNATSSSEGSTVDVAPPREGEQAEIEPEEDLKPE
 ACFTEGCIKKFPFCQVSTEEGKGKIWMNLRKTCYSIVEHNNWFETFI VFM I
 LLSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQT
 YFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRLRPLRAL S
 RFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVN
 MTTGSMFDMSEVNNFSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATF

FIG. 5

KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGV
 IIDNENQOKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPKQKPIPRPANKFQ
 GMVDFVTRQVFDISIMILICLNMVTMMVETDDQSKYMTLVLSRINLVFI
 VLFTGEFLLKLLISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS
 PTLFRVIRLARIGRILRLIKGAKGIRTLFALMMSLPALFNI GLLFLVM
 FIYAIFGMSNFAYVKEAGIDDMFNFTFGNSMICLFQITTSAGWDGLLA
 PILNSAPPCDPAIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVNMY
 IAVILENFSVATEESAELSEDDFEMFYEVWEKFDPDATQFIEFCKLSDF
 AAALDPPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGE
 MDALRIQMEDRFMASNP SKVSYEPIITTLKRKQEEVSAAIQ RNYRCYLL
 KQRLKNI SN TYDKETIKGRIVLP IKGDMVIDKLN GNSTPEKTDGSSSTIS
 PPSYDSVTKPDK EKFEKDKPEKESKGEV

SEQ ID NO:3

TGAAAAGATGGCCCGAGCACTGCTGGTA CCCCCGGGACCTGAGAGCTTCC
 GCCTTTTCACTCGAGAACTCTTGCTGCTATCGAAAAGCGTGTGCAGAA
 GAGAAAGCCAGAAACCCAGAAAGAACAGACATTGACGATGAGAACAA
 GCCAAAGCCAAACAGTGA CTGGAAGCTGGGAAGACCTTCCA TTTATCT
 ATGGAGACATTCCTCCAGAGATGGTGTGGAGCCTCTGGAGGACCTGGAC
 CCTACTACGT CAGTAAGAAAAC TTTGTAGTGTGAATAAAGGGAAGGC
 AATTTTTCGATT CAGTCCACCTCCGCTTGTATATTTTAACTCCACTAA
 ACCCGTTAGGAAAATTGCTATTAAGATTTGGTACACTCTTTATT CAGC
 ATGCTTATCATGTGCATATTTTGACCAACTGTGTATTATGACATTGAG
 CAATCCTCCTGACTGGACGAAGATGTAGAGTACACATTCAC TGGGATCT
 ATACCTTTGAGTCACTATAAAGATCTTGGCCAGAGGATCTCTGCTTAGAA
 GATTTCACAATTTCTCGTGACCCATGGAAC TGGCTGGATTT CAGTGT CAT
 CGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGC
 TGAGAACGTT CAGAGTTCTCCGAGCAATTGAAAACAATATCAGTCATTCCA
 GGTTTAAAGACCATCGTGGGGGCCCTGATCCAGTCGGTGAAGAGCTGTC

FIG. 5

TGACGTCATGATACTCACTGTGTCTGTCTGAGCGTCTTTGGCTCTCATCG
GGGTGCAGCTCTTCAATGGCAACCTGAGGAATAAATGCTTGCACTGGCCT
CCAAGCGATTCTGCTTTTGAGATCAACACTACTTCCCTACTTCAATGGCAC
AATGGACTCAATGGGACATTTGTTAATGTAACAATGAGCACATTTCAACT
GGAGGACTAATTCGCAGATGACAGCCACTTTTATGTTTGGATGGACAA
AAAGATCCTTTACTTTGTGGAATGGTCCGATGCAGGACAAATGTCCAGA
AGGTAACATCTGTGTGAAGCTGGACGAAACCCCAACTACGGTTACACGA
GCTTTGACACATTTAGCTGGGCTTCTTATCGCTGTTTCGACTCATGACT
CAAGACTACTGGAGAACCTTTACCAGTTGACATTTACGTGCAGCTGGGAA
AACTACATGATCTTTTTCGTCTCTGTTAATTTCTTTGGGCTCATTTTATT
TGGTGAACTTTGATCTCTGGCTGTGTGGTGGCCATGCGCTATGAGGAAACAAAT
CAGGCCACACTGGAGGAGGCTGAGCAGAAAGAGGCGGAGTTTTCAGCAGAT
GTTGGAGCAGTTGAAAAAGCAGCAAGAGGAGGCTCAGGCGGTGGCAGCTG
CCTCAGCAGCGTCCAGAGACTTCAGTGGGATAGGAGGTTAGGAGAACTT
CTGGAGAGTTCTTTCAGAAAGCTTCCAAGTTGAGCTCCAAGAGTGCCAAAGGA
GTGAGGGAATCGAGGAAAGAAAGAGGAGACAGAGGAGGACACTTGGAGGAA
ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAATCAGAAAGACAGC
GTCAAGCGAAGGAGTTTCTGTCTCTCCCATCAGTCTCTCTTGTAGTATCCGTGGCT
CGACAAGAAGCTGTGCTCTCCCATCAGTCTCTCTTGTAGTATCCGTGGCT
CCCTGTTTCCCAAGACGCAATAGCAAAACGAGCAATTTTCAGCTTCAGA
GGTCGGGCGAAGGACGTGGGTCTGAGAAATGACTTTGCGGATGATGAACA
CAGCACCTTTTGAAGATAGCGAGAGCAGGAGAGACTCACTGTTTGTGCGGC
ACAGACCTGGAGAGCGACGCAACAGTAACGTTAGTCAAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGTTTCTTGGGTACCACCACTGAAACAGAACTCA
GGAAGAGAAAGCTAAGTTCTTACCAGATCTCGATGGAATGCTGGAGAT
TCTCTGGGAGACAAAGAGCCATGAGCATAGCCAGTATCTTGACCAACAC
GATGGAGGAACCTTGAAGAACTTAGACAGAAAGTGTCCACATGCTGGTATA
GATTTGCCAATGTGTTTTTGATCTGGGACTGTTGTGAATCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATTTGTATGGATCCATTTGTTGACCTGGC
CATCACCATCTGTCATCGTTTAAACACACTGTTTCATGGCCATGGAGCACT
ATCCCGATGACGAGCAGTTTCAGCAGTGTGCTGACGCTGGGAAACCTGGTC
TTCACCGGGATCTTCAAGCGGAGATGGTCTGAAATCATCGCAATGGA
TCCCTATTACTATTCCAGAGGGCTGGAATATCTTTGATGGAATTAATG

FIG. 5

TTAGCCTGAGTTTAATGGAGCTTGGCCCTGGCAACCGTGGAGGGGCTGTCC
 GTGCTTCGGTCTCTCAGACTGCTCGAGTCTTCAAGTTGGCAAAATCCTG
 GCCACACTGCAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCAC
 TGGGCAACCTGACCCCTGGTGTGCCATCATCGTCTTCATTTTGGCGTG
 GTCGGCATGCACTGTTTGGAAAGAGCTACAAGGAGTGTGTTCAGAGAT
 CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
 CCTTCTGATAGTGTTCGCGTGTCTGTGGGAGTGGATAGAGACCATG
 TGGGACTGCATGGAGGTCCGGGCCAGACCATGTGCCCTTATTTGTGTAT
 GTTGGTCATGGTGATTTGGAACTTGTGGTCTTGAACCTTCTCTGGCCT
 TATTGTGTGTTCTTTAGTTCAGACAACTTGTCTGTGCTACGGACGATGAT
 AACGAAATGAACAACCTCCAGATCGCGTGGGAAGGATGCAAAAGGGGAT
 TGATTAATGTGAAAAATAAGATACGGGAGTGTTCGGAAGCGTTTITTA
 GAAAGCCGAAAGTGTAGAAATCCACGAAGGAAACAAAATAGACAGCTGC
 ATGTCCAATAACACGGCGGTAGTTGAAATAAGCAAGAGCTTAACACCT
 TAAAGACGGTAACGGAACCAACAGTGGGTGGGTACTGGAAGCAGTGTGG
 AGAAATA CGTAATTGATGAATAATGACTACATGTCAITCATCAACAAACCC
 AGCCTCACCGTGACGGTGCCAAATTGCCGTGGGAGAGTCTGACTTTGAAAA
 TTTAAACACGGAAGAGTTTAGCAGTGAATCAGAACTGGAAGAAAGCAAGG
 AGAAATTAAATGCAACCCAGCTCTTCTGAAGGAAGCACAGTTGACGTTGCT
 CCGCCCCGGAAGGTGAACAAGCTGAAATGAACCTGAGGAGGACCTTAA
 GCCAGAAGCTTGTCTTTACTGAAGGATGCATTAATAAAATTTCCCTTCTGCC
 AAGTAAGTACGGAAGAAAGGTAAAGGAAATACTGGTGAATCTTAGGAAG
 ACCTGCTATAGCATTGTGGAACACAACTGGTTTGAGACGTTTCAATGTGTT
 CATGATTTCTCTCAGTAGTGTGCTTTGGCCCTTTGAAGATATATACATTG
 AGCAACGGAAGACCATCAAAACCATGCTGGAGTATGCTGACAAAGTCTTC
 ACTTACATCTTCACTCTGGAAATGCTCCTCAAATGGGTGGCCTATGGATT
 TCAAAACCTAATTTACCAATGCTGCTGGTGGTTGGACTTCTTGATTGTTG
 ATGTTTCTTTTGGTTAGCCTGGTGGCCAAACGCTCTTGGCTATTCAGAACTT
 GGTGCCATCAAAATCCCTACGGAACCTGAGAGCTCTGAGGCCGCTCCGAGC
 CTTATCCCGCTTTGAAGCATGAGGGTGGTTGTGAACGCTCTTGTGTGGTG
 CAATCCCTCCATCATGAATGTGCTACTGGTGTGCCCTCATCTTCTGGTTA
 ATCTTTAGTATCATGGGTGTAATCTGTTTGTCTGGAAGTTTCTATCACTG
 TGTTAACATGAACAACGGGCAGCATGTTCCGACATGAGTGAAGTCAACAATT
 TCAGCGACTGTCTAGGCTCTTGGCAAGCAAGCCCGATGGAAAGATGTGAAA

FIG. 5

GTCAACTTTTGACAAATGTTGGGGCTGGCTACCTGGCAATTGCTGCAAGTGGC
 CACATTCAAAGGCTGGATGGATATTATGTATGTCAGCTGTGGATTCAAGGG
 ACGTCAAACTGCAGCCTGTATATATGAAGAAAATCTGTACATGTATCTGTAC
 TTTTGTATCTTTCATCATCTTTGGTCTCTTCACTCTAAATCTATTCAT
 CGGGCTCATATAGACAACCTTCAACCCAGCAGAGAAAGATTGGAGGTC
 AAGACATCTTTATGACAGAGAGCAGAAAAGTACTACAATGCAATGAAG
 AAACTTGGCTCCAAAACCTCAGAGGCCATCCCTCGACCTGCAAAACA
 ATTTCAAGGAATGGTCTTTGACTTTGTAAACAGACAAGTGTGTGACATCA
 GCATCATGATCTCTCATCTGCCCTCAACATGGTGAACCATGATGGTGGAAACG
 GACGACAGAGCAAAATACATGACCCCTGGTTTTGTCCCGAATCAACCTGGT
 ATTTCATCGTCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCA
 GATACTACTACTTCAAGATTGGCTGGAAACATCTTTGACTTTTGTGGTGGTG
 ATTCTCTCAATTGTAGGAATGTTCTTGTCTGAGCTGATAGAGAAAGTATTT
 TGTGTCTCTACCTCTTCCGAGTCACTCCGCTGGCCAGGATGGACGAA
 TCCTAGCCTGATCAAGGCGCCAAAGGGATCCGCAAGCTGCTCTTTGCT
 CTGATGATGTCCTTCTTGGCTGTTCAACATCGGCTCTGCTTTTCCT
 CGTCATGTTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCCTATGTTA
 AAAAAGAGCTGGAAATTGATGACATGTTCAACTTTGAGACTTTTGGCAAC
 AGCATGATCTGCTGTTCCAAATCACCACTCTCGGGCTGGGATGGACT
 GTTGGCCCCATCTCAACAGTGCACCTCTGACTGTGACCCCTGATGCAA
 TTCACCTGGAAGCTCAGTGAAGGAGACTGTGGGAACCCATCTGTGGGG
 ATTTTCTTTTGTGAGCTACATCATATATCTTCTGTTGTGGTGAA
 CATGTACATGCTGTCTCTGGAGAACTTCAGCGTTGCCACAGAGAAA
 GTGCAGAGCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGTCTGG
 GAGAAGTTGAGCCCTGAGCCACCCAGTTCTATAGAGTCTTGCAAGCTCTC
 TGACTTTGAGCTGCCCTGGATCCTCCCTCTCTCATCGCAAGCAAAACA
 AAGTCCAGCTCATTGCATGGACCTGCCCATGGTGAAGTGGAGCCGCATC
 CACTGCCCTGGACATCTTATTTGCTTTTACAAAGCGGCTCCTGGGTGAGAG
 TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGTTTCATGGCTT
 CCAATCCCTCCAAGTCTCTTATAGAGCCATTACCACTCTCTGAAGGC
 AAACAAGAGAGGTTGCTGTCTATCATTTAGAGTAAATACAGATGTTA
 TCTTTTAAAGCAAGGTTAAAAACATATCAATACGTATGACAAAGAGA
 CAATCAAGGGGAGGATGTCTTGGCTATATAAAGGAGATATGGTTATTGAC
 AAATTAAATGGGAATTCACCCCAAGAAAAGACAGATGGGAGTTCTCTTAC

FIG. 5

CACCTCCCTCCTTCCTATGACAGTGTAAACAAAACCCAGATAAGGAAAAGT
TTGAGAAAAGACAAACCAGAAAAAGAAAGCAAAAGGGAAGAGGTCTGAGAG
AATCAAAAAGTAAAAAACAACAAAACAAAAAATTTCAAAAATTTAAAAAGG
AAACAAAGAAATGTCTTTGTAAATCAATTTGTTCACAGCCTCTGAAGGTAAA
GTGTCCGTGTCAACTGGACTC

SEQ ID NO:4

Genbank® GI No.: 19923380; Ref No.: NM_006922.2; Homo sapiens sodium channel, voltage-gated, type III, alpha (SCN3A), mRNA

AGCGAAGCGGAGGCATAAGCAGAGAGGATTCCTGGAAAAGGTCTCTTTGTGTTTCTTATCCACAGAGAAAGAA
AGAAAAAAATGTAACTAAATTTGTAAACCTCTGTGGTCAAAAAAAGGCTGAAACAGC
TGCCAGAGGAGACACAGTTTATACCTTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAAGG
CTCTGTTTTATCAGAGATTATGGAGCAAGAAAACCTAGCAAGCCACATCAAGGTTTGACAGGGATGAG
ATACCTGTCAAGGATTCAATAGTAGAGTGGCTTACTGGGAAAGGACAAAGAAATCTCTTCTAGGGATATTG
TAAGAATAAATGAGATAAATTCACAGAGGGACCTGGAGCTTTTCCGGAAGAAAGGTGCTGTGACTATCTAA
GGTAATTCGTATGCAAGAAGCTACACGTAATTAATGTGCAGGATGAAAAGATGGCACAGGCACCTGTTGG
TACCCCCAGGACCTGAAAGCTTCGCGCTTTTACTAGAGAATCTCTTGTGCTATCGAAAAAACGCTGTGC
AGAAGAGAAAGCCAAAGAGCCAAAAAGGAACAAGATAATGATGATGAGAAACAAACCAAGGCCAAATAGT
GACTTGGAAGCTGGAAAGAACCTTCCAATTATTTATGGAGACATTCCTCCAGAGATGGTGTGAGAGCCCC
TGGAGGACCTGGATCCCTACTATATCAATAAGAAAACCTTTATAGTAATGAATAAAGGAAAGGCAATTTT
CCGATTCAGTGCACCTCTGCTTGTATATTTAATCTCCACTAACCCCTGTAGGAAAAATTGCTATCAAG
ATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCATATTTTGACCAACTGTGTATTTATGACCT
TGAGCAACCCCTCCTGACTGGACAAAGAAATGTAGAGTACACATTCACCTGGAATCTATACCTTTGAGTCACT
TATAAAAATCTTTGGCAAGAGGTTTTGCTTAGAAGATTTTACGTTTCTTCTGTGATCATGGAACCTGGCTG
GATTTGAGTGTGATGGCATAATGTGAAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAA
CAATTCAGAGTTCTCCGAGCACTGAAAACAATTTCAATTCAGTCATTCAGGTTTAAAGCCATTTGTGGGGCCCT
GATCCAGTCGTTAAAGAGCTTTCTGATGTGATGATCTGCTGATCTGTGCTGTCTGAGCGTGTCTGCTCTC
ATTTGGCTGCACTGTTTCATGGGCAATCTGAGGAATAAATGTTTGCATGGCCCCCAAGCAATTTGCTTT
TTGAAACCAACACCTTCTTAAATGGCAATGGATTCAAATGGGACATTTGTGTTAATGTAAACAAT
GAGCACATTTAACTGGAAGGATTAATTGGAGATGACAGTCACTTTTATGTTTGGATGGGCAAAAAAGAC

FIG. 5

CCTTTACTCTGTGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTC
 GAAACCCCAACTATGGCTACCAAGCTTTGACACCTTTAGCTGGGCTTTCTGTCTCTATTTTCGACTCAT
 GACTCAAGACTAATGGGAAAATCTTTTACAGTTGACATTAAGTGTCTGTGGGAAAACAATACATGATATTT
 TTTGTCTGGTCAATTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTGTGGCTGTGTGGCCATGGCCT
 ATGAGGAGCAGAAATCAGGCCACCTTGGAAAGACAGAACAAAAAGAGGCCGAATTTACAGCAGATGCTCGA
 ACAGCTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGGGCAGCATCAGCTGCTTCAAGAGATTTTCAGT
 GGAGTAGGTGGTTAGGAGAGCTGTTGAAAAGTTCTTCAGAAAGCATCAAAGTTGAGTTCCAAAGGTGCTA
 AAGAATGGAGGAACCGGAGGAAGAAAAGACAGAGAGAGACCTTGAAAGGAAAACAACAAAGGAGAGAG
 AGACAGCTTTCCAAATCCGAATCTGAAGACAGCGCTCAAAGAAGCAGCTTCCCTTTCTCCATGGATGGA
 AACAGCTGACCGAGTGACAAAAAATCTGTCTCCCTCATCAGTCTCTCTTTGAGTATCCGTGGCTCCCTGT
 TTTCCCAAGACGCAATAGCAAAAACAAGCAATTTTCAGTTTCAGAGGTCGGGCAAGGATGTTGGATCTGA
 AAATGACTTTTGTGATGATGAACACAGCACATTTGAAGACGGCAAGCAGAGAGAGACTCACCTGTTTGTG
 CCGCAGACATGGAGAGCGACGCAACAGTAAAGTTAGTCAGGCCAGTATGTATCCAGGATGGTGCCAG
 GGCCTCCAGCAAAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGTTTCTTTGGTGGTGGACC
 TTTAGCTTAACGTACCTACTGGAACAATTTCCCCAGAGGCCACCACTGAAACGGAAAGTCAGAAAG
 AGAAGTTAAGCTCTTACAGATTTCAATGGAGATGCTGGAGGATTTCTCTGGAAAGGCAAGAGCCGTGA
 GCATAGCCAGCAATTTGACCAACACAAATGGAAGAACTTGAAGAACTAGACAGAAATGTCGCGCCATGCTG
 GTATAGATTTGCCAATGTTCTTTGATCTGGGACTGCTGTGATGATGTTAAAGATGTTAAACATCTTTGTG
 AAATTAATTTGTTATGGATCCAATTTGTGATCTTGCCATCACTATTTGCATTTGCTTAAATFACCCCTCTTTA
 TGGCCATGGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTGACTGTAGGAAAACCTGGTCTTTTAC
 TGGGATTTTACAGCAGAAAATGGTTCTCAAGATCATTTGCCATGGATCCTTATTTACTATTTCCAAAGAGC
 TGGAAATATCTTTGATGGAAATTAATGTGAGCTTCAAGTTTAAATGGAGCTTGGTCTGTCAAATGTGGAGGAT
 TGTCTGTACTGCGATCATTCAGACTGCTTAGAGTTTCAAGTTGGCAAAATCCTGGCCCACTAAATAT
 GCTAATTAAGATCATTTGGCAATTTCTGTGGGGCTCTAGGAAACCTCACCTTGGTGTGGCCATCATCGTC
 TTTCAATTTTGTGTGGTGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAAATGTGTCTGCAAGATCAATG
 ATGACTGTACGCTCCACGGTGGCAGATGAACGACTTCTTCCACTCCTTCCATGATTTGTTCGCGTGTCT
 GTGTGAGAGTGGATFAGAGACCATGTGGGACTGTATGGAGTGGTGGCCAAACCATGTGCTTATTTGT
 TTTATGTTGGTTCATGGTTCATTTGGAAAACCTTGTGGTCTGAACCTCTTTCTGGCCTTATTAATGAGTTTCA
 TTAGCTCAGACAAACCTTGTGCTACTGATGATGACAAATGAATGAATAATCTGCAGATTTGCAGTAGGAAG
 AATGCAAAAGGGAATTTGATTAATGTGAAAATAAGATCGGGAGTGTTCCAAAAAGCCCTTTTGTAGAAAG
 CCAAAAGTTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGTCATGCCAATAATATCTGGAATTTGAAA
 TAAGCAAAAGAGCTTAATATCTTAGAGATGGGAATGGAAACCAAGTGGTGTAGGTACTGGAAGCAGTGT
 TGAAAATACGTAATCGATGAAAATGATTAATGTCTATTCAATAACAAACCCAGCCCTCACCGTCACAGTG
 CCAATTTGCTGTGGAGAGTCTGACTTTTGAAAACCTTAAATACTGAAGAGTTTCAGCAGTGTGAGAACCTAG

FIG. 5

AAGAAAGCAAGAGAAATTAATGCAACCACTCATCTGAAGGAAGCAGATTGATGTTGTTCTACCCCG
 AGAAGGTGAACAAGCTGAACCTGAAACCGAAGAGACTTTAAACCGAAGCTTGTTTACTGAAGGTGT
 ATTAAGAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAGCAAGGAAGATCTGTGGAATCTTCGAA
 AAACCTGCTACAGTATTGTTGAGCACAACTGGTTTGAGACTTTTCAATTGTTTCATGATCCTTCTCAGTAG
 TGGTGCAATTGGCTTTGAAGATATATACATTGAACAGCAAGAGACTATCAAAACCACTGCTAGAATATGCT
 GACAAAGTCTTTACCTATATATTCACTCTGGAATGCTTCTCAATGGGTGCTTATGGATTTCAAAACAT
 ATTTCACTAATGCTTGGTGGCTAGATTCTTTGATCGTTGATGTTCTTTGGTAGCCCTGGTAGCCAA
 TGTCTTGGCTACTCAGAACTCGGTGCCATCAAATCAITTAAGGACATTAAGAGCTTTAAGACCTCTAAGA
 GCCTATCCCGTTTGAAGGCATGAGGTGGTGTGAATGCTCTTGTGGAGCAATCCCTCTATCATGA
 ATGCTGTTGGTCTGTCTCAATCTTCTGTTGATCTTTAGCATCATGGGTGTAATTTGTTGCTGGCAA
 GTTCTACCACTGTGTTAAATGACAAACGGGTAAACATGTTTGACATTAAGTATGTTAAACAATTTAGTGAAC
 TGTTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAACGTAAGAGTAAACCTTGATAATGTTGGCGCTGGCT
 ATCTTGCACTGCTCAAGTGGCCACATTTAAAGGCTGGATGGATATTAATGATGCAGCTGTTGATTCAAG
 AGATGTTAAACCTCAGCTGTATATGAAGAAATCTGTACATGTTTATATCTTTGTCTATCTTTATCATC
 TTTGGGTCAATCTCACTCTGAATCTATTCAATGTTGTTGTCATCATAGATAAATCTCAACAGCAGAAAAAGA
 AGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAATATTAAATGCAATGAAGAAACTTGG
 ATCAAGAAACCTCAGAAACCCATACCTCGCCAGCAACAAATTCGAAGAAATGGTCTTTTGATTTGTATA
 ACCAGACAAGTCTTTGATATCAGCATCAATGATCCTCATCTGCCTCAACATGGTCACCATGATGGTGGAAA
 CGGATGACCAAGGCAATACATGACCTAGTTTGTCCCGGATCAACCTAGTGTTCATTTGTTCTGTTTAC
 TGGAGAATTTGTGCTGAAGCTGTTTCCCTCAGACACTACTTCTCATATAGGCTGGAACATCTTTGAC
 TTTTGGTGGTGAATCTCTCCATGTAGGTATGTTTCTGGCTGAGATGATAGAAAAAGTATTCTGTGTCCTC
 CTACCTTGTTCGAGTGTATCCGTCTTGGCAGGATGGCCGAATCCTACGTCTGATCAAGGAGCAAGGG
 GATCCGCAAGCTGCTCTTTGCTTTGATGATGTCCTTCTCGCTGTTTAAACATCGGCCTCCTGCTCTTC
 CTGGTCAATGTTTATCTATGCCATCTTTGGGATGTCCTTCTGCTATGTTTAAAGGAAGCTGGAAATTG
 ATGACATGTTCACTTTGAGACCTTTGGCAACAGCATGATCTGTTGTTCCAAATTAACAACCTCTGCTGG
 CTGGGATGGAATTGCTAGCACCTATTCTTAATAGTGCACCAACCGACTGTGACCTTGACACAATTCACCCCT
 GGCAGCTCAGTTAAGGAGACCGTGGGACCATCTGTGGGATTTCTTTTGTGAGTTACATCATCA
 TATCTCTTCTGTTGTTGTTGAACATGATCATCGCGGTGATCTCGGAGAACTTCAGTGTGCTACTGAAGA
 AAGTGACAGAGCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAAAAGTTTGTATCCCGAT
 GCGACCCAGTTTATAGAGTTCTTAAACTCTCTGATTTTGACAGTGCCTGGATCCCTCTCTTCTCATAG
 CAAAAACCAACAAAGTCCAGCTTATTTGCCATGGATCTGCCCATGGTCAGTGGTACCGGATCCACTGTCT
 TGATATTTTATTTGCTTTTACAAAGCGTGTGTTGTTGAGAGTGGAGAGATGGATGCCCTTCGAATACAG
 ATGGAAGACAGGTTTATGGCATCAAAACCTCCAAAGTCTTATAGGCTTATTACAAACCACTTTTGAAC
 GTAAACAAGAGGAGGTGTCTGCCGCTATCATTTAGCGGTAATTTAGATGTTATCTTTTAAAGCAAGGTTT

FIG. 5

AAAAATATATCAAGTAACTATATAAAGAGGCAATTAAAGGAGGAGTTGACTTACCTATATAAAACAAGAC
ATGATTTATTTGACAAACTAAATGGGAATCCACTCCAGAAAAAAGATGGAGTTCCCTTACCAACCCCTC
CTCCTTCCCTATGATAGTGTAAACAAAACAGAACGAAAGTTGAGAAAGACAAACCAAGAAAAAGAAAG
CAAGGAAAAAGAGTCAGAGAAAAATCAAAAGTAAAGAAACAAAGAAATATCTTTGTGATCAATTTGTTT
ACAGCTATGAAGGTAAAGTATATGTTGTTCACTGGACCTTCAAGAGGAGTCCATGCCAAACTGACTGTTT
TAACAAATACTCATAGTCAGTGCCTATATAAAGACAGTGAAGTGACCTCTGTCTCACTGCAACTCTGTGAA
GCAGGTATCAACGTTGACAAGAGTTGCTGTTTTTATTTACCAGCTGACACTGCTGAGGAGAAAAACCAAT
GGCTACCTAGACTATAGGATAGTTGTGCAAGTGAAACATTTGTAACCTACCAAAACACCTTTAGTACAGT
CCTTGCACTCCATTTATTTTAACTTCCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCAATTTCC
ATGTTCCCAATTCATAGTTTATTCATAAATGCTATGTCATACTTTTGTGAAATGAGGTTTACGTTGAAGA
AACAGTATACAAGAACCTGCTCTCAATGATCAGACAAAGGTGTTTTGCCAGAGAGATAAAATTTTGG
CTCAAAACCAAGAAAAAGAAATGTAATGGCTACAGTTTCAGTTACTTCCATTTCTAGATGGCTTTAAATTT
TGAAAGTATTTTAGTCTGTTATGTTTGTCTATCTGAACAGTATATGTCCTGTAAGCTCTCTCTAAATA
TTTTAAGGATTTATTTATGCAAGTATTTCTGTTTCAGCAAGTGCAAAATTTATTTCTAAGTTTTCAGAGCT
CTATATTTAATTTAGTCAATGCTTTCCAAAAGTAAATCTAATAAATCCATTTAGAAAAATATATCTA
AAGTATGCTTTAGAAATAGTTGTTCCACTTTCTGCTGCAGTATGCTTTGCCATCTTCTGCTCTCAGCAA
AGCTGATAGTCTATGTCAAATTAATACCTATGTTATGTAATAGTTATTTATCTGTTGGTGCATGTTT
GGGCAATATATATATAGCCTGTATAAACAACCTTCTATTAATCAAAATATGACCAAGTATATGTCCTT
TTGCAAGCTTCCAAAGGATGATCTGTCATCTCAATCCATCTTCAAGCTTGGTTAAAGAAATGTCAC
TGTTAATATTTGCCATGCTCTATTTTACTCAATCCATCTTCAAGCTTGGTTAAAGAAATGTCAC
ATATTGGTGATAGAAATTCACCTGCTGTCCTCATATGTCAGAGCAATTAATTTGAAGCTATTTTAC
AAACACCTTTTACTTTTCACTTTTAAATTCACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAA
CACACTGGATCTGCTCACTGACAAAAACCTATTTCTTCAATTTTGCTAAAAATATGCTAAAAACCTTGT
AAATATAAATAATGTAAATAATTAATCAACTTTATTTGTGTCAGCATTTTGTACATAAGAAAAATTTTCA
GGTTGATGACATCACAATTTATTTTACTTTTACTTTTGTCTTTTGTATTTTAAATCAAAATCCAACTTT
TGAATCCATAAGATTTTCAATGGATAATTTCCATAAATAAAGTTAGATAATGGGTTTATGGATTTCT
TTGTTATAATATATTTTCTACCAATTCATAGGAGATACATTTGGTCAAACTCAAACTCAGATCAATTT
CTACCACTATGTTGGCTCAATAAACCTTTTATTCATAGATGTTTTTTTTTTTATTTTCACTTTGTAGTA
TTTACGTATGACACTAGTCTTATTTTTTTTAAATCTGCTGCACTAAAGCTATTAACAATATAACATGGA
CTTTGTCTTTTTTGGCATGAACAAAGTGGCAAGTTGTGCAATTAACCTAACATGATATAAATTTTTTGT
TTTTGCACAAAACCAAAAGTTTAAAGTTAAATCTTTTTTACAAACTATTTACTGTAGTATTAAGAACT
GCAATGAGGGAATTTGCTATTTGCTAAAAAGAAATGGTGAGCTACCTATTTTGGAGCCAAAAAGAAATTT
CAATTTTATTTGCAATTTCACTTATTTGGGCTCTGGGGTTTTTTTTTTTTTTTTTTTTTTGCTGTGGCAGTTTA
AAATATATATAATTAATAAACCCTGTGCTTGTGATCTGACATTTGTATATACATAAAGTTTACATGAATTTTA

FIG. 5

CAACAACTAGTGTGATGATTCACCAAGCAGTACTACAGAACAAAGGCAAAATTAAGAGCAGCTTTGTGAAC
TTTTATGTGTGCAAGGATCAAGTTCCATGTTCCAACTTTCAGGTTTGATAATAAGTAGTAACCAACC
TACAATAGCTTCAATTTCAATTAACCTCCCTGGCTATAAGCATCAAACTCATCTCTTTCAATATAAT
TGATGCTATCTCCTAATTAATCTGGTGGCTAATAATGTTACATCTTTGTTACTTAAATGCATTATATAA
ACTCCTATGTATACATAAGGTATTAATGATATAGTATTGAGAAATTATATAACTTTTTTCAAGAAC
CCTTGGATTTATGTGAGGTCAAAACCAAACTCTTATTTCTCAGTCGAAAACTCCAGTTGTAATGCATATTT
TTAAAGACAAATTTGGATCTAAATATGTATTTTCAATAATCTCCATAATAAATATATATAAGGTGAAAAA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO:5

GenBank® GI No.:19923381; Ref. No.:NP_008853.2; sodium channel, voltage-gated, type III, alpha; sodium channel, voltage-gated, type III, alpha polypeptide [Homo sapiens]

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKPKKEQDNDENKPKPNSDLEAGKNLPFIYDIPP
EMVSEPLEDLDPYYINKKTFIVMNGKAI FRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILT
NCVFMTLSNPPDWTKNVEYFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDPSVIVMAYVTEFVDLG
NVSALRFRVLRAKTTISVIPGLKTI VGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLOW
PPSDSAFETNTTISYFNGTMSNGTFVNVTMTSTFNWKDYIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFSLFRIMTQDVWENLYQLITLRAAGKTYMTFFVLVIFLGSFYLVNLIL
AVVAMAYEEQNQATLEAEQKEAEFQOMLEQLKQEEAQAVAAASAAASRD FSGVGLGELLESSSEASK
LSSKGAKENRRNRKRQRREHLEGNNGERDSFPKSESEDSVKRS SFLF SMDGNRLTSDKKFCSPHQSLL
SIRGSLFSPRRNSKTSIFSFRGRADV GSENFADDEHSTFEDGESRRDSLFPVPHRHGERNSNVSQASM
SSRWVPGIPANGKMHSTVDCNGVVSIVGGPSALTSPTGQLPPEGTTTETETVRKRLSSYQISMEMLEDSS
GRQAVSTASILLTNTMEEL EESRQKCPPCWYRFANVFLIWDCCDAWLKVXHLVNLIVMDPFVDLAIITICI
VLNTLFWAMEHYPMTEQFSSVLTVGNLVFTGIFTAEWVLKIIAMD PYYFQEGWNIFDGIIVSISLMELG
LSNVEGLSVLRSFRLIRVFKLAKSWPTLNMLIKIIGNSVGALGNLTVLAIIVFIFAVVGMQLFGKSYKE
CVCKINDDCTLPRHNMNDFHSLIVFRVL CGEWIETMDCMEVAGOTMCLIVFMLVMVIGNLVVLNLF
ALLLSFSSDNLAAATDDDNEMNLQIAGVRMQGIDYVKNMRECQKAFRRKPKVIEIHGNKIDSCMS
NNTGIELSKELNLRDNGTTSVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLNTTEEF
SSESELEESKEKLNATSSSEGSTVDVVI.PREGEAETEPEEDFKPEACFTGCIKKKFPFCQVSTEEGKGK

FIG. 5

IWNLRKTCYSIVEHNWFETIVFMILSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWV
AYGFQTYFTNAWCWLDLIVDVSLVSLVANALGYSEIGAKISLRTLRALRPLRALSRFEGMRVVVNALVG
AIPSIMNVLLVCLIFWLIFSIMGVNLFAKFPYHCVMNMTGNMFDISDVNNLSDCOALGKQARWKNVKVNF
DNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGVIIDN
FNQQKKFGGQDIFWTEEQKXYNAMKKIGSKKPQPIPRPANKFQGMVDFVTFQVFDISIMILICINM
VTMMVETDDQKYMVLVSRINLVFIVLFTGEFVLKLVSLRHYFTIGWNI FDFVVVILSIVGMFLAEMI
EKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLFALMMSLPALFNIGLLLFVLMFIYAI FGMNFAYV
KKEAGIDDMFNFTFGNSMICLFQITTSAGWDGLLAPILNSAPPCDPTIHPGSSVKGDRDPSVGIF
FVSYIIISFLVVVNMYTAVILENFSVATEESAEPLEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAAL
DPPLLI AKENKQOLIAMDLP MVSGDRJHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNP SKVS YEP
ITTTILKRKQHEVSAAI IQNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKLGNGNSTPEKTDG
SSSTTPPPSYDSVTKPKDKKFEKDKPEKESKGKEVRENQK

SEQ ID NO:6

GenBank® GI No.: 12642271; GB No.:AF225986.1; Homo sapiens voltage-gated sodium channel alpha subunit splice variant SCN3A-s (SCN3A) mRNA, complete cds, alternatively spliced

AGCGAAGCGGAGGCATAAGCAGAGAGGATTC TGGAAGGTCTCTTGTGTTTCTTATCCACAGAGAAAGAA
AGAAAAAATGTAACTAATTTGTAAACCTCTGTGCTCAAAAAAAGCTGAAACAGC
TGCCAGAGGAAGACACGTTATACCCTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAGG
CTCTGTTTATCAGAGATTATGGAGCAAGAAACCTGAAGCCAAAGCCACATCAAGGTTTGACAGGGATGAG
ATACCTGTCAAGGATTCATAGTAGTGGCTTACTGGGAAAGGAGCAAGAAATCTCTTAGGGATATTG
TAAGATAAATGAGATAATTCAAGAGGGACCTGGAGCTTTCCGAAAAAGGTGCTGTGACTATCTAA
GGTAATTCGTATGCAAGAAGCTACACGTAATTAATGTGCAGGATGAAAAGATGGCACAGGCACTGTTGG
TACCCCCAGGACCTGAAAGCTTCGCTTTTACTAGAGAACTCTTGTCTGCTATCGAAAAACGTGCTGC
AGAAAGAGAAAGCCAAAGGCCAAAGAGCAAGATAATGATGATGAGAACAAACCAAGCCAAATAGT
GACTTGGAGAGCTGGAAAGAACCTTCCATTTATTTATGGAGACATCTCCAGAGATGGTGT CAGAGCCCC
TGGAGGACCTGGATCCCTACTATATCAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGCAATTTT
CCGATTCAAGTCCACCTCTGCCTTGATATATTTTAACTCACTAAACCCTGTTAGGAAAAATTGCTATCAAG

FIG. 5

ATTGTTGGTACATTTCTTTATTTACGATGCTTTATCATGTGCACTATTTTGGACCAACTGTGTATTTATGACCT
 TGAGCAACCCCTCTGACTGGACAAAGAAATGTAGAGTACACATTCACGTGGAATCTATACCTTTTGAGTCACT
 TATATAAAATCTTGGCAAGAGGGTTTTCCTTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTG
 GATTTTCAGTGTCAATTGTGATGGCAATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTTGAGAA
 CATTCAGAGTTCTCCGAGCCTGAAAAACAATTTTCAGTCAATCCAGGTTTAAAGACCAATGTGGGGGCCCT
 GATCCAGTCGGTAAAGAGCTTTCTGATGTGATGATCCTGACTGTCTCTGCTGAGCGTGTCTTGTCTCTC
 AATTGGGCTGCAGCTGTTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGGCCCCCAAGCGATTCCTGCTT
 TTGAAACCAACACACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTAAATGTAAACAAT
 GAGCACAATTTAATGGAAAGGATTAATTTGGAGATGACAGTCACTTTTATGTTTGGATGGGCAAAAAGAC
 CCTTTACTCTGTGGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAAGGATACATCTGTGTGAAGGCTGGTC
 GAAACCCCAACTATAGGCTACACAAGCTTTTGACACCTTTAGCTGGGCTTTCTCTGTCTCTATTTTCGACTCAT
 GACTCAAGACTATTTGGGAAAATCTTTTACCAGTTGACATTAACGTGTGCTGTGGGAAAAACATACATGATATTT
 TTTGTCTCTGCTCATTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTGTGGCTGTGGTGGCCATGGCCT
 ATGAGGAGCAGATCAGGCCACCTTGAAGAAGCAGAACAAAAAGAGGCGGAATTTTCAGCAGATGCTCGA
 ACAGCTTAAAAAGCAACAGGAAGCTCAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTTCAGT
 GGAGTAGGTGGTTTAGGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGGTGCTA
 AAGAAATGGAGGAACCGGAGGAAGAAAAGACACAGAGAGCACCCTTGAAGGAAAACAACAAAGGAGAGAG
 AGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAGAAGCAGCTTCTTTTCTCCATGGATGGA
 AACAGACTGACCAGTGACAAAAAATCTGTCCCTCATCAGTCTCTCTTGAGTATCCGTGGCTCCCTGT
 TTTCCCAAGACGCAATAGCAAAAACAAGCATTTTCAGTTTCAGAGGTGCGGCAAGGATGTTGGATCTGA
 AAATGACTTTTGTGATGATGAACAACAGCACAATTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTGTG
 CCGCACAGACTGGAGAGCGGACGCAACAGTAAACGGCAACCACTGAACCGGAAGTCAGAAAGAGAAAGGT
 TAAGCTCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAAGGCAAGAGCCGTGAGCATAGC
 CAGCATTCAGCAACACAAATGGAAGAATCTTGAAGAATCTAGA CAGAAATGTCCGCCATGCTGGTATAGA
 TTTGCCAAATGTGTTCTTGATCTGGGACTGCTGTGATGCAATGGTTAAAGTAAACAACATCTTGTGAATTTAA
 TTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTCATGTTCTTAAATACCCCTTTTATGGCCAT
 GGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTGACTGTAGGAAACCTGGTCTTTTACTGGGAT
 TTTACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTAATTTCCAGAAGGCTGGAATA
 TCTTTGATGGAAATATTGTACAGCTCAGTTTAAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTTGTCTGT
 ACTGGGATCAATTCAGACTGCTTAGAGTTTCAAGTTGGCAAAATCCTGGCCCCACACTAAATATGCTAAAT
 AAGATCAATGGCAATCTGTGGGGCTCTAGGAAACCTCACCTTGGTGTGGCCATCATGCTCTTCATTT
 TTGCTGTGTGGCCATGAGCTCTTTGGTAAAGAGCTACAAAGAAATGTGTCTGCAAGATCAATGATGACTG
 TAGCTCCCAAGGTGGCACAATGACATCTTTCCACTCCTTCTGATGTGTTCCGCGTGTGTGGGA
 GAGTGGATAGAGACCATGTGGACTGTATGGAGGTGCTGGGCCAAACCATGTGCTTATTTGTTTTCATGT

FIG. 5

TGGTCATGGTCATTGGAAACCTTTGTGGTTCCTGAACCTCTTTCTGGCCTTATTATTAGTTTCATTTAGCTC
AGACAACTTTGCTGCTACTGATGATGACAAATGAATAATCTGCAGATTGCAGTAGGAAGAAATGC
AAGGGAATTTGATTATTGTGAAAAATAAGATCGGGAGTGTTCAAAAAGCCCTTTTGTGAAAAGCCAAAAG
TTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGCATGCTCCAAATAATACTGGAATTGAAATAAGCAA
AGAGCTTAATTATCTTAGAGATGGGAATGGAACCAACAGTGGTGAGGTACTGGAAGCAGTGTGTGAAAA
TACGTAATCGATGAAAATGATTATATGTCAATTCATAAACAAACCCAGCCTCACCGTCA CAGTGCCAAATTG
CTGTTGGAGAGTCTGACTTTTGAACCTTAAATACTGAAGAGTTTCAGCAGTGAGTCAGAACTAGAAAGAAAG
CAAAGAGAAATTAATGCAACCACTCATCTGAAGGAAGCAGCAGTTGATGTTGTTCTACCCGAGAAAGGT
GAAACAAGCTGAAACTGAAACCGGAAGAAGACTTTAAACCGGAAGCTTGTTTTACTGAAGGGTGATTAAAA
AGTTTCCATTCTGTCAAGTAAGTACAGAAAGGCAAGGAAGATCTGGTGGAATCTTCGAAAAACCTG
CTACAGTATTGTTGAGCAAACTGGTTTGAGACTTTTCATTGTGTTCTATGATCTCTTCAGTAGTGTTGCA
TTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAACCATGTAGTAATATCTGACAAAG
TCTTTACCTATATATTCATTTCTGGAATGCTTCTCAATGGGTGCTTATGGAATTTCAAACATATTTTCA
TAATGCCGTGGTGGCTAGATTCTTGATCGTTGATGTTTCTTTGTGTAGCCTGGTAGCCAAATGCTCTT
GGCTACTCAGAACTCGGTGCCATCAAAATCATACGGACATTAAGAGCTTTTAAAGACCTCTTAAAGAGCCTTAT
CCCGTTTGAAGGCAAGAGGTGGTTGTGAATGCTCTTGTGTGAGCAATCCCTCTATCAATGAATGTGCT
GTTGGTCTGTCTCATCTTCTTGTGTTGATCTTTAGCATCATGGGTGTGAAATTTGTTTGTGGCAAGTTCTAC
CACTGTGTTAAATGACAAAGGGTAAACATGTTTGAATTTAGTATGATGTTAAACAAATTTGAGTGAATGTCCAG
CTCTTGGCAAGCAAGCTCGGTGGAAAAACCTGAAAGTAAACCTTTGATAATGTTGGCGTGGCTATCTTGC
ACTGCTTCAAAGTGCCACAAATTAAGGCTGGATGGAATATTATGATGCACTGCTGTTGATTCACGAGATGTT
AAACTTCAGCCTGTATATGAAGAAAATCTGTACATGTATTTATACCTTTGTCATCTTTATCATCTTTGGGT
CAATCTTCACCTGTGAATCTATTCTTGGTGTCTATCAWAGATAACTTCAACAGCAGCAGAAAAAGAAATTTGG
AGGTACAGACATCTTTATGACAGAGGAACAGAAAAAAATTAACAATGCAATGAAGAAACTTGGATCCAAAG
AAACTTCAGAAAACCAATACTCGCCCAAGCAAAACAAATTCGAAGGAATGGTCTTTGATTTGTAAACCAAGAC
AAGTCTTTGATATCAGCAATCATGATCTTCATCTGCCCTCAAACATGGTACCATGATGGTGGAAAAACGGATGA
CCAGGGCAAAATACATGACCTTAGTTTGTCCGGATCAAACCTAGTGTTCATGTTCTGTCTACTCTGGAGAA
TTTGTGCTGAAGCTCGTTTCCCTCAGACACTACTACTTCACTATAGGCTGGAAACATCTTTGACTTTTGTGG
TGGTGAATCTCTCCATTGTAGGTAATGTTTCTGGCTGAGATGATAGAAAGTATTTCTGTGTCCCCCTACCTTT
GTTCCGAGTGATCCGCTTTGCCAGGATTTGCCGGAATCCCTACGCTCTGATCAAAGGAGAAAGGGATCCCG
ACGCTGCTCTTTGCTTTGATGATGTCCTCTCTCGCTGTGTTTAAACATCGGCCCTCCTGCTCTCTCTGGTCA
TGTTTATCTATGCCATCTTTGGGATGTCAACTTTGCTGATGTTTAAAGGAAGGAGCTGGAATTTGATGACAT
GTTCAACTTTGAGACCTTTGGCAACAGATGATCTGCTGTTTCCAAATTAACAACCTCTGCTGGCTGGGAT
GGATTGCTAGCACTTATCTTAATAGTGTGACCAACCGGACTGTGACCCCTGACAAATTCACCCCTGGCAGCT
CAGTTAAAGGAGACCGCTGGGGAACCCATCTGTTGGGAATTTCTTTTTTGTGAGTTTACATCATCATATCTCTT

FIG. 5

CCTGGTTGTGTGAACATGTACATCGGGTTCATCTCGGAACTTCAGTGTGTGCTACTGAAGAAAGTGCAGAGCCCTGAGTCAGGATGACTTTGAGATGTTCTATGAGGTTGGGAAAGTTTGATCCCGATCGGACCCAGTTTATAGAGTTCCTAAACTCTCTGATTTGAGCTGGCTGGATCCTCTCTTCATAGCAAAACC
 CAACAAAGTCAGCTTATGCGCATGGATCTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATT
 TTATTTGCCCTTACAAAGCGTGTGTTGTGAGAGTGGAGAGATGGATGCCCTTCGAAATACAGATGGAAG
 ACAGGTTTATGGCATCAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAACGTAAACA
 AGAGGAGGTGTCTGCCGTATCATTCAGCGTAAATTTTCCAGATGTTGACTTACCTATAAACAAGACATGATTA
 ATATCAAGTAACTATAACAAGAGGCAATTAAGGGAGGATGACTTACCTATAAACAAGACATGATTA
 TTGACAAACTAAATGGGAACCTCCACTCCAGAAAAACAGATGGGAGTTCTCTACCACTCTCCTCCTTC
 CTATGATAGTGTAAACAAACAGACAAAGGAAAGTTTGGAGAAAGACAAACAGAAAAAGAAAGCAAGGA
 AAAGAGGTCAAGAAAAATCAAAAGTAAACAAAGAAATTAATCTTTGTGATCAAATGTTTACAGCCT
 ATGAAGGTAAAGTATATGTGTCAACTGGACTTCAAGAGGAGGTCCATGCCAAAATGACTGTGTTTAAACAAA
 TACTCATAGTCAGTGCCTATAAAGACAGTGAAGTACCTCTCTGTCACTGCAACTCTGTGAAGCAGGGT
 ATCAACGTTGACAAAGAGGTGCTGTTTTTATACAGCTGACACTGCTGAGGAGAAACCAATGGCTACC
 TAGACTATAGGATAGTTGTGCAAAAGTGAACATGTAACACACCAACACACTTTAGTACAGTCTCTGCA
 TCCATTTCTATTTTAACTTCCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCAATTTCCATGGTCC
 CCAATTCATAGTTTATTCATATGCTATGTCATATTTTGTAAATGAGGTTTACGTTGAAGAAACAGTA
 TACAAGAACCCCTGCTCTCAAAATGATCAGACAAAGGTGTTTGGCCAGAGAGATAAAATTTTGTCTCAAAA
 CCAGAAAAAGAAATGTAATGGCTACAGTTTCAGTTACTTCCATTTCTAGATGGCTTTAAATTTTGAAGT
 ATTTTAGTCTGTTATGTTTGTCTATCTGAACAGTTATGTGCTGTAAAGTCTCCTCTAATAATTTAAAG
 GATTAATTTTATGCAAAAGTATCTGTTTCAGCAAGTGCAAAATTTTATTTCTAAAGTTTCAGAGCTCTATATT
 TAAATTTAGGTCAAATGCTTTCCAAAAAGTAATCTAATAATCCATTCTAGAAAAATATATCTAAAGTATT
 GCTTTAGAAATAGTTGTTCCACTTTCTGCTGAGTATGCTTTTGCCATCTTCTGCTCTCAGCAAAAGCTGAT
 AGTCTATGTCAATTAATAACCTATGTTATGTAATAATGTTATTTATCCTGTGGTGCATGTTTGGGCAAA
 TATATATATAGCCTGATAAACAACTTCTATTAATCAAAATGTAACCAAGTATGTTAAAGGCTATCACTAATGCAATGTAAT
 CTTCCAACAGGATGATCCTGTATCATTCATTAACATAGTTTAAAGGCTATCACTAATGCAATGTTAAT
 ATTGCCATAGTGTCTATTTTACTCAATCCATTTCTCAAGTCTTGGTTAAAGATGTCACATATTGG
 TGATAGAAATGAATCAACCTGCTCTGTCATATGTCAGCAGAAATAATTTGAAGCTATTACAAACACC
 TTTACTTTTTGCACTTTTAAATCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAAACACACTG
 GATACTGCCTACTGACAAACCTATTCTTTCATATTTTGTCTGCAATTTTGTACATAAGAAATATTTTTCAGGTTGAT
 AATAATGTAAAAATAAATCAACTTTTATTTGTGCAATTTTGTACATAAGAAATATTTTTCAGGTTGAT
 GACATCACAATTTATTTTACTTTTATGCTTTTGTGATTTTAAATCACAATTTCCAAACCTTTTGAATCC
 ATAAAGATTTTCAATGGATAATTTCCATAAATAAAGTATGATTAATGGGTTTTTATGGATTTCTTTGTTAT
 AATATATTTTTCTACCATTCCAATAGGAGATACATTTGGTCAAAACACTCAAAACCTAGATCATTTTCTACCAA

FIG. 5

AAAGCGTCTGTGAGAGAGAAAGCCAAAGAACCCAAAGAAAGAGCAAGACATTGACGATGAGAAACAAACCA
 AAGCCAAACAGCGACTTGAAGCTGGGAAGAACCTTCCATTATCTATGAGAGACATTCTCTCCAGAGATGG
 TGTGACAGCCCTTGAGGACCTGGACCCCTACTATGTGAGTAAGAAACCTTTGTAGTGTGAATAAAGG
 GAAGCGATTTTTCGATTGAGTTCAGCGCCACCTCCGCCCTGTATATTTAACTCCGCTAAACCCCTGTTAGGAAA
 ATTGCATTAAAGATTTGGTACACTCTTTGTTGAGCATGCTTATCATGTGCACTATTTTGACCAACTGTG
 TATTTATGACGTTGAGTAATCCTCCGACTGGACAAAGATGTAGAGTATACGTTCACTGGGATCTATAC
 CTTTGAGTCACTTATAAAGATCTTTGGCAAGAGGTTTGGCTTAGAAGATTTCACTTTCTCCGTGACCCA
 TGGAACTGGCTGGATTTGAGTGTGATCGTGATGGCATAATGTGACAGAGTTTGTGGACCTGGGCAATGTCT
 CAGCGCTGAGAACCTTTCAGAGTTCTCCGAGCATTGAAACAAATATCAGTCATTCCAGGTTTAAAGACCAT
 CGTGGGGCCCTGATCCAGTCCGTGAAGAGCTGCCGACGTGATGATCCTCACCGTGTCTGTCTCAGT
 GTCTTTGCTCTAATCGGGCTGCACTCTTTCATGGGCAACCTGAGGAATAAATGCTCGCAGTGGCCCCCGA
 GCGATTCGGCTTTTGAAAACCAACACTACTTCTCTACTTCAATGGCACAAATGGATTCAAATGGGACATTTGT
 TAATGTAAACAATGAGCACTTTCAACTGGAAGGATTTATATCGCAGATGACAGTCACTTTTATGTCTTGGAT
 GGACAAAAGATCCCTTTACTCTGTGGAATGGCTCCGATGCAGGACAATGTCAGAGGGTACATCTGTG
 TGAAGGCTGGACGAAACCCCACTACGGCTACACAAGCTTTTGACACCTTCAGCTGGGCCCTCTTGTCCCT
 GTTTCGACTCATGACTCAGGACTTACGGGAGATCTTTACAGTTGACATTCGCTGCGTGGGAAACC
 TACATGATATTTTTCGTCTGTGTAATTTTCTTGGGCTCGTTTATTTGTTGAACTTGATCCTGGCTGTGG
 TGGCATGGCCTATGAGGAGCAGAACCGGCCACACTGGAGAGGCTGAAACAGAGGAGGACAGATTTCA
 GCAGATGCTGGAGCAACTGAAGAGCAGCAGGAGGAGGCTCAGGCATGGCTGCAGCCCTCGCGGCATCC
 AGAGACTTCAGTGAATAAGAGGTTAGGAGAACTTCTGGAGAGTTCTTCAGAGCTTCCAAAGTTGAGCT
 CCAAGAGTGTAAAGAGTGGAGAACCGGAGGAAGAGAGAGACAGAGGGAACACTTGGAGGGAAACCA
 CAGAGCGGATGGAGACAGGTTTCCAAAGTCGGAATCGGAAGACAGTGTCAAACGAAGAAGCTTCTCTGCTC
 TCCCTGGATGGCAACCCGCTGACTGGTGACAAAGAGCTGTGCTCTCCCAAGCTCTCTCTTGAGTATCC
 GTGGTCCCTGTTTTCCCAAGAGCAATAGCAAAACGAGCAATTTTCAGCTTCAGAGGTGGGCGGAAGGA
 CGTGGGTTCTGAGATGACTTTGACAGATGAGCAGCACCCTTCGAGGACAGCGAGCAGGAGCAGGAGAC
 TCCCTGTTTGTGCCGACAGACCTGGAGAGCGACGCAACAGTAAACGTAACCACTGAAACGGAAAGTCA
 GGAAGAGAAGGCTAAGTTCTTACAGATTTCAATGAAATGCTGGAGGATTCCTCTGGAAGACAAGATC
 CATGAGCATAGCCAGTATCCTGACCAACACCATGGAGGAACCTGAAGAACTAGACAGAGTGGCCACCA
 TGCTGATATAGATTCGCCAATGTGTTTTTGTACTGGGACTGTGTGATGATGATGTTAAAGTGAAGCATC
 TTGTGAATTTAATGTGATGGATCCATTTGTGTATCTTGGCAATAACAATTTGATCGTATTAATAACACT
 GTTTCATGGCCATGAGGACATATCCCATGACCCAGCAGTTTCAGCAGTGTGCTGACTGTGGGAAACCTGTGTC
 TTCACTGGGATCTTTCACAGCCGGAATGTTCTTAAATCATTTGCCATGGACCCCTATTATTTATTTCCAAAG
 AGGGCTGGGAATATTTTCGATGGAATTTTGTAGCCTGAGTTTAATGGAGCTAGGCCCTGGCAAAATGTGGA
 GGGGCTGTCTGTGCTTCGGTCTTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAAGTCTCTGGCCCCACACTG

FIG. 5

AACATGCTCATTAAAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCTGGTGGTGGCCATCA
 TCGTCTTCAATTTTGGCGTGGTGGGCAATGAGCTGTTGGAAAGAGCTACAGGAGTGTGTCTGCAAGAT
 CAATGTGGACTGCAAGCTGGCGGTGGCACATGAACGACTTCTTCCACTCCTTCCCTGATCGTGTTCGGA
 GTGCTGTGTGGGAGTGGATAGAGACCATGTGGGACTGCATGGAGGTGCGGGCCAGACCATGTGCCCTTA
 TTGTGTTTCATGTTGTTCAATGTTGGAACTTGTGGTTCTGAACTCTTCTTGGCCCTTATTTGTTGAG
 TTCTCTTAACTTCAATTAACCTTGTCTACTGACGATGATAACGAAATGAACAACCTCCAGATCGCGGTG
 GGAAGGATGCAAAAGGGAATTTGTTGTAATAAAGATACGGGAGTGTTCGGAAGAGCTTTTCA
 GAAAGCCGAAAGTGTATAGAAATCCAAAGAGGCAACAAAATAGACAGCTGCATGTCCTCAATAACACGGGCAT
 CGAATTAAGCAAGAGCTTAACTTAAAGACGGTAATGGAACCAACGAGCGGTGGGAACCGGAAGC
 AGTGTGGAAAAATACGTAATCGATGAAAAATGACTACATGTCAATCATATAAACAATCCAGCCTCACCGTGA
 CTGTGCCAATGCTGTGGGAGTCTGACTTTGAAAAATTTAAATACGGAAGAGTTTCAAGCTGATGTTGCTCCA
 ATTGGAAGAAAGTAAGGAGAAATTAATGCAACCCAGCTCTTCTGAAGGAAGCACAGTTGATGTTGCTCCA
 CCCGAGAGGTGAACAAGCAGAAATTAACCTGAGGAGGACCTTAAGCCAGAAAGCTTGTTTTACTGAAG
 GGTGCATTAAAAAATTCCTTCTGTCAAGTAAGTACAGAAGAGGTAAGGAAAAATATGTTGGAATCT
 TAGGAAGACATGCTACAGCATTTGGAGCACAACTGGTTTGGAGACATTCATTGTGTTTCAATGATCTCCTC
 AGTAGTGGCGCTTTGGCTTTGAGGATATATACATTGAGCAACGAAAGACGATCAAGACCATGCTGGAGT
 ATGCAGACAAGGTCTTCAAGTACATCTTCACTCTGGAGATGCTCTCAATGGGTGGCCATGGAATTTCA
 AACCTAATTCACCAATGCTGGTGTGGTTGGACTTCTGATCGTTGATGTTTCTTTGGTTAGCCCTGGTA
 GCCAATGCTTGTGGTTACTCAGAACTTGGTGGCCATCAAACTCCAGGACACTGAGAGCTCTGAGGCCGC
 TCCGAGCCTTATCCGCTTTGAAGCATGAGGTGGTTGTAATGCTCTTGTGGTGAATTCCTTCCAT
 CATGAATGTGTTATTTGGTGTCTCATCTTCTGGCTGATTTTGTAGCATCATGGGTGTGAATCTGTTGCT
 GGAAAGTTCTATCACTGTGTTAACAGCAACAAGGCAACATGTTTGAATAAAGAAAGTGAACAATTTCA
 GTGACTGTTCAGGCTCTTGGCAAGCAAGCCCGGTGGAAGAAATGTGAAGTCAACTTTGACAAAGTTGGGC
 TGGCTACCTGGCATTTGTCAGAGTGGCCACATTCAAAAGGCTGGATGGACATCATGTATGCAGCTGTTGAT
 TCCGGGAAGTCAAACTGAGCCCATATATGAAGAAAAACCTGTACATGTACCTGTACTTTGTCTATCTTCA
 TCATCTTGGCTCGTCTTCACTCTAAATCTATTCATCGGTGTCATCATAGACAACCTTCAACCCAGCAGAA
 GAAGAAGTTTGGAGTCAAGACATCTTTATGACAGAAAGACAGAAGAAATACTACAATGCAATGAAGAAG
 CTCGGCTCAAGAAACCTCAGAAGCCCATCCCTCGGCCCTGCAAAACAAATTTCAAGGATGGTCTTTTGATTT
 TTGTAACAGACAAAGTGTTTGACATCAGCATCATGATCTCTATCTGCCCTCAACATGGTGAACCATGATGGT
 GGAACGGATGACAGAGCAAAATACATGACCTGGTTTGTCCGGAATCAACCTAGTGTTCATTTGTCTC
 TTACATGGGGAGTTTCTGTGAAGCTCATCTCCCTCAGATACTACTTTCACGATAGGTTGGAACATCT
 TTGACTTTGTGGTGTGATTTCTCTCGATTTGTAGGAATGTTTCTCGCAGAGCTGATAGAGAAGTATTTCTGT
 GTCCCTACCTGTTCCGAGTCACTCCGCTGGCCAGGATGGACGAATCTCTACGCTGATCAAGGGGCC
 AAGGGATCCGCACTGTCTCTTTGCTTTGATGATGTCCCTTCTCGGCTGTCTTCAACATCGGCCCTCCTGC

FIG. 5

TTTTCTGGTCATGTTTCATCTACGCCATCTTTGGGATGTCAACTTTGCCATATGTTAAAAAGAGGCTGG
 AATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCTGTTTCCAATCACCACCTCT
 GCCGCTGGGACGGACTGCTGGCCCCCATCTCAACAGCGCACCTCCGACTGTGACCCCGATGCAATTC
 ACCCTGGAAGCTCGGTGAAGGGACTGTGGAAACCCATCCGTGGGATTTCTTTTGTGTCAGCTACAT
 CATCATATCTTCTCTGGTGGTGAACATGTACATCGCTGTCTCTCTGGAGAACTTCAGCGTCGCCACC
 GAAGAAAGTGCAGAGCCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAAGTTCCGACC
 CTGACGCCCATCTCAGTTTCATAGAGTTCTGCAAGCTTTCTGACTTTTGCACTGGCCCTGGATCCTCCCTCCT
 CATCGCAAGCCCAACAAAGTCCAGCTCATTTGCCATGGACCTGCCATGTGAGTGGAGACCGCATCCAC
 TGCCTGGACATCTTGTCTTTTACAAGCGGTCTTGGCGAGAGTGGAGAGATGGACGCTCTTCGAA
 TCCAGATGGAAGATCGCTTCATGGCTTCCAACCCCTCCAAGTCTCTTATGAGCCCATTTACCACCCCT
 GAAACGGAAACAAGAGGAGGTGTCTGTCTATCATTCAGCGTAATTATAGATGTTATCTTTTAAAGCAA
 CGGTTAAAAACAATATCGAGTAAATACGACAAGAGACAATCAAGGAAGGATTGACTTTGCCCTATAAAG
 GAGATATGGTTATTGACAAATTTGAATGGGAATCCACCCAGAAAGACGGATGGGAGTTCTCCACAAC
 CTCTCCTCTTCCCTATGACAGTGTAAACAAACAGATAAGGAAAAGTTTGAGAAAGACAAACCCAGAAAAA
 GAAATCAAAGGGAAGAGGTGAGAGAGATCAAAAGTAAAAAGAGACAAAGAAATGTCTTTGTAATCAAT
 TGTTTACAGCCTCTGAAGGTAAAGTATCCGTCTCAACTGGACTTAAGGAGAGGTCCATGCCAAACTGAC
 TGTTCACAAATACTCAAGGTGAGTGCCTATACAGACAGTGACCTCTGTCACTGCCACTCTGTGAGAC
 AGGTATCAACATTGACAAGAGGTGTCTGTCTCCATTACAGCTGACACTGTCTGAGGAGAACTCCATTGT
 GCAAGTGACCCGTCATCATGCCCCCAACTCCCATTAGTACAAAGCTCTGTCTCATCTATTTTAAACATICA
 CATTTGGCCATATTTTACAAAACTGTCTCCAGTGTATCTTCTGTGGTCCCCTTCTATAGTCTGTTCATAA
 TACTATGTCACTATTTTGTAAATGAAGTTTACGTTAAGGAAAAATATATATATAAGAAATCCCATGTTGC
 TAAGTCCACAAGTTTCTCCAGTAATCATAAAAAATAATTTTGCCCTGAGAGATGAAATTTATTGCTCAAAAC
 AAAAAAAATAAATCTAAATGTTAAACAGTTTC

FIG. 5

SEQ ID NO:9

GenBank® GI No.:6981510; Ref. No.:NP_037251.1; sodium channel, voltage-gated, type III, alpha polypeptide [Rattus norvegicus]

MAQALLVPPGESFRLFTRESLAAIEKRAAEKAKPKKEQIDDDENKPKNSDLEAGKNLPFIYGDIPP
 EMVSEPLEDLDPYVSKKTFVVLNKGKAI FRFSATSALYILTPINPVRKIAKILVHSLFMSLMIMCTILT
 NCVFMTLSNPDPWTKNVEYTFGTGIYTFESLIKILARGFCLEDFTFLRDPNNWLD FSVIMAYVTFVDLG
 NVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKLSVMILTVCLSVFALIGLQLFMGNLRNKCQW
 PPSDAFETNTSYFNGTMDNSGTFVNVTMTSTFNWKDYIADDSHFYVLDGQDPLLCGNGSDAGQCPEGY
 ICVAGRNPNGYTSFDTFSWAFISLFRMTQDYWENLYQLTLRAAGKTYMIFVVLVFLGSFYLVNLIL
 AVVAMAYEEQNQATLEEAQEKAEAFQOMLEQLKKQEEQAQAAAAAASRD FSGIGLGELLESESSK
 LSSKSAKEWRNRKRRQREHLEGNHRADGRFPKSESDSVKRRSFLLSLDGNPLTGDKKLCSPHOSLL
 SIRGSLFSPRRNSKTSIFSFRGRAKDVSEND FADDSHSTFDESRRDSL FVPHRPGERRNSNGTTTET
 EVRKRRLSSYQISMEMLEDSSGRQSRMSIASILTNTMEELEESRQKCPWCYRFANFVLWDCCDAMLKV
 KHLVNLIVMDPFVDLAITICIVILNTLFMAMEHYPMTQQFSVLT VGNLVTGIFTAEMVLKIIAMDYVY
 FQEGWNIFDGIIVSLMELGLANVEGLSVLRFRLLRVFKLAKSWPTLNMLIKIIIGNSVGALGNLTIVL
 AIIIVFAVGMQLFGKSYKECVCKINVDCKLPRWHMNDFFHSFLIVFRVLCGEWETMWDCEVAGQTM
 CLIVFMLVMVIGNLVNLFLALLSSFSNDNLAAATDDNEMNNLQIAVGRMQGIDFVKNKIRECFRKA
 FFRKPKVIEIQEGNKIDSCMSNNTGIEISKELNYLKDNGTTSVGVTGSGSVKVIDENDYMSFINNPSL
 TVTVPIAVGESDFENLT EEFSESELEESKEKLNATSSSEGSTVDVAPREGGEQAEIPEEDLKPEACF
 TEGCIKKFPFCOVSTEEGKGIWNMLRKTCSIVEHNWFETFI VFMILLSSGALAFEDIYIEQRKTIKTM
 LEYADKVFTYIFILEMLLKWVAYGFQYFTNACWLDFLIVDVSVLSIVANALGYSEIGAIKSLRTIRAL
 RPLRALSRFEGNRVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGNMFEIKEVN
 NFSDQALGKQARWKNVKNFDNVGAGYLALI QVATFKGWMIMYAAVDSRDVKLQPIYEENLYMYLYFV
 IFIIFGSFFTLNLFIGVIIDNFNQKKKFGGQDIFWTEQKKKYNNAMKKLGSKKPQKPIPRPANKFQGMV
 FDFTRQVFDISIMILICLNMVTMMVETDQSKYMTLVSRLNLFVILFTGEFLKLISIRYYFTIGW
 NTFDVVVILSI VGMFLAELEKIFVSPTLFRVIRLARIGRILRLIKGAKGIRTLIFALMMSLPALFNIG
 LLLFLVMFTYALFGMSNFAYVKEAGIDDMNFETFGNSMICLFQITTSAGWDGLLAPILNSAPDCDDPD
 AHPGSSVKDCGNPSVGIFEFVSYIIISFLVVNNMYIAVILENFSVATEESAEPIS EDDFEMFVEVWEK
 FDPDATQFIEFKLSDFAALDPPLLIAKENKVLIAMDLPMVSGDRHCLDILFAFTKRVLGESGEMDA
 LRIQMEDRFWASNP SKVSYEPTITTLKRQEEVSAIIQRNYRCYLLKQRLKNISSKYDKETIKGRIDLIP
 IKGDMVIDKLNGNSTPEKTDGSSSTTSPPSYDSVT KPDKEKFEKPEKEIKGKEVRENQK

FIG. 5

SEQ ID NO:10]

GenBank® GI No.:9055329; Ref. No.:NM_018732.1; Mus musculus sodium channel, voltage-gated, type III, alpha polypeptide (Scn3a), mRNA

TTTTTATATCTGTGAGTGACGAAAGAAAAAGAAAAAGAAATGC AAAATGTTGAG
 CCCAGTTAATGTCAGGATTTTAATCAATTC AATTCTATTGGAGAACTACTTTAAAGCATGTAGAAGC
 TGAGGATAGTGGTCATATCTTAACACCAAGTACTTGGGAGGTGAAGCCAGAGAACTAGCCTAGATTAC
 TCTCAGATATATTGTAAGTTTGAGGCTAGCCTGGGCTACATGA AACTGTATCTCATCCACACATAAAAA
 AAGTTTGATATATTGGTATATTAAACAATGATATAACAAA AIGTTTAGAATTATAGCAAAAATAATTGG
 TAAAAGTACCTACTATATATATATATATATATACATATATATACATATATATGTATACATATATACATATAT
 GTATTTTAAATTTAACATAAGCTTTTAAAAATCGAATTATCTTACCTTTTAAAGAGAAATGTAATTCA
 TATTTCAACATTCCTTTCAGTTTCTAGAGTAGAATCTGAAGTGACAGTTGATGCATTAGTAGTGTCTGTT
 GTGTGCATCTGTCTGTCAATCCATCCACGCTTTGCCACCTGTAAATTAGAGACCTTTTACACAGGCAAG
 GGGCCAGAGGCTCGCGCAGTCTGTAATTAAAGTATTAATTTTCTTAGTCGATCTAAAATGAAAAATA
 AGTAAATCTAAAATTAGATTTATAAAGAAAAAATGTGCTGAATAA ACGACTTGATTTTCAACCTTAATA
 TTATTAACACCTTTTGTGTAATTTCAITACAGCTGCGAGTCTTCAAGTTGGCAAAATCCTGGCCACACTGAAT
 TACTCATTTAAGATCATCGGCAACTCGGTGGGCGCACTGAGTGTGGA AAGAGCTACAAGAGTGTGTTCCGCGTG
 ATGTCATTTTCCGCTGGTGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTGCAAGATCAA
 CGAGGAGTCAAGCTCCCGCGCTGGCACATGAACGACTTCTCCACTCTTCTGATAGTGTCCGCGTG
 CTGTGTGGGAGTGAGATAGAGACCATGTGGGACCTGAGGTGCGGGCCAGACCATGTGCTTATTG
 TGTATTATGTTGTCATGTTGTTGGAACTTGTGGTCTGAACTTTCTGGCCCTTATTGTTGAGTTC
 CTTTAGCTCAGACAACTTGTGCTACGGACGATGATAACGAAATGAACA AACTCCAGATCGCGTGGGA
 AGGATGCAAAAGGGATGATTATGTGAAAAATAAGATACGGGAGTGTCTCCGAAAGCCCTTTTITAGAA
 AGCCGAAAGTATAGAAATCCACGAAGGAAACAAAATAGACAGCTGCATGTCC AATAACACGGGCGTAGT
 TGAATAAGCAAGAGCTTAACCTTAAGACGGTAAACGAAACCA CCAAGTGGCGTGGGTACTTGGGAGC
 AGTGTGGAGAAATAGTAATTGATGAAAATGACTACATCATTCATCA AACAACCCAGCCTCACCGTGA
 CGGTGCCAATJTGCCGTGGGAGAGTCTGACTTTGAAAATTTTAAACA CCGAAGAGTTTAGCAGTGAGTCAGA
 ACTGGAAGAAAGCAAGGAGTAAGCGCTTTTTCAGTTTCAGGCCACCACTTTTGGCCAATCTACACAGTA
 TGGCTCTCTGTATTGTTTTTGGCTGTGAGGTGCTTAATCAACAGAAAGAAATGGGTTGGGTGTGTAG
 CTCAGGGGATAGGATACCTTAGCATGCATGACGTCTTGTAGTACCCCAACAC CACCCCAAAAGCAACTTA
 AACGTAGATAAAGTTGGAACATCATGAGAAATGGGTAAGTTCGTTTAAATATAA CTTTCCCATAGGAAAT

FIG. 5

CACAACTTGAGCGATTAAATGTTTCATTTCTTGATAAATGAAAGCCGTGATTTAAATATGCAATCCTAAC
AAAAGAGATACATTTAAACACATTTTCCCTGCTAGTTATTTGTTTGTAGAAAACCTCAATGAACATATATT
TTAAATGGTGGTATGCCATCACGTGTGAAAAATTTACATAGCTCTTATTACATTTAAAGTGTTTTATTAC
AATTTGTTTACTAGGAAGGTCAGCCATACCTGATATTTTCCATTAAAGATGAGCAAACTATGACAT
TTTCTACATTAACCTTAAATACTGAAGATTAAACATTTGATGATTAATGAGATCTACAGATGGGAAAT
TTCCGTCAATATGAGTAGTTGATCGAATGAAAGAGAAAATTTTCATATGCTATGATTTGAGCTCAATTGG
GTCTAATGACAAATAGCTTAGTGACATTACCTTCAATATTTTATTTATTTATTTATTTATTTATTTGATGT
AACAGCTGGAGGTTAATCTAGCACAGATGGTGTATAAAGGATCTCTAGCTGGAGGGAATCCTCAACACC
CTGGAACAGACCAGATGTTTGTATCTATGGATTTCTCTGGAGCTTTTGAAAAACCAAGTTACACCAAGAT
AATTTGCTCTAGAAATCCTTATAGAAATTTATGGCATCAAACTCACAGTGGTCCCATTTCTTTTCATAT
TTTGAATAATGTTTAAACCTAATAAACAATATGAACAAAATGAGGTAGCAATGTTTATTTTACAGTTGC
ACACTAATTTGTCATAGCACATCTAATTTACGTTGCTCATCTCTAGTCTAGTAAAGATCAATTTCTGGCTTTA
TTTTCTATCACCTGGCGTAGAATTGACTTACAAAGAACCTTAGAGGCTAGCAGGCAATTCAGTACTAT
TTTTCTCAAATTCGTCACAAAGACAGTCTTTATCAAGTGTGTTCCCAACAACTCATAACTCATTAACATC
TATTTAATTGATCTACAGGCGGTGTTTAAATTTTAGGCGTTTAAAGATGGGAAGGAGGTTAAATGAC
AGAAATTTGAATGAGGCTCAATATTTGGGTACATCGTTTAAAAAGTGGAAAGATACCTGTTCTCCAAAGGA
GAGCAGGTTGATAATGAGCTCTGTTTATCTCAGGCGAGTGGAGAGCAGGAGACAGGCAAAAGGATGTGC
CGGTGTCTGGAAGCTCCAGACTGCAGCCTTGACAGATAACTCGGAGCTTGGAAATTTCTGTCATGTTCA
CGAAGGAGTCTCTAAACAGAAAGCAATTAGAAAGGGGTATCCTAGGAACATCTGTATTATTAAGAGTAA
GGACCTTAGACTGAGAGATAATGGAGATTAACTTACACTGTTATAGCAATGAGATGGTGAATTTCTGG
GCCAAAATAATAGAGAACCAAGCGTAATTGGCAATTTACAGACCTCAAGAACTCTGAGGAATCAGAAAGT
GGCAATTCACCTGTCTGATAAGGGCTTCTGAGGAAGGTCAACAGGTTTGTATGGAAGGAATTC

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MLKIIGNSVGALGNLTLLVLAIIIVFIPAVVGMQLFGKSYKECVCKINEDCKLPRWHMNDFFHSLIVFRV
LCGEWETWDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFALLLSFSSDNLAAATDDNEMNNLQIavg
RMQKIDYVKNKIRECFRKAFFRKPKEIHEGNKIDSCMSNNTGVVEISKEINYLKDNGNTTSGVGTGS
SVEKXVIDENDYMSFINNPSSLIVTVPIAVGESDFENLNTTEEFSSSELEESKEVSALFSSGHHFCAIYTV
WLLCIVFCL